

BEST AVAILABLE COPY

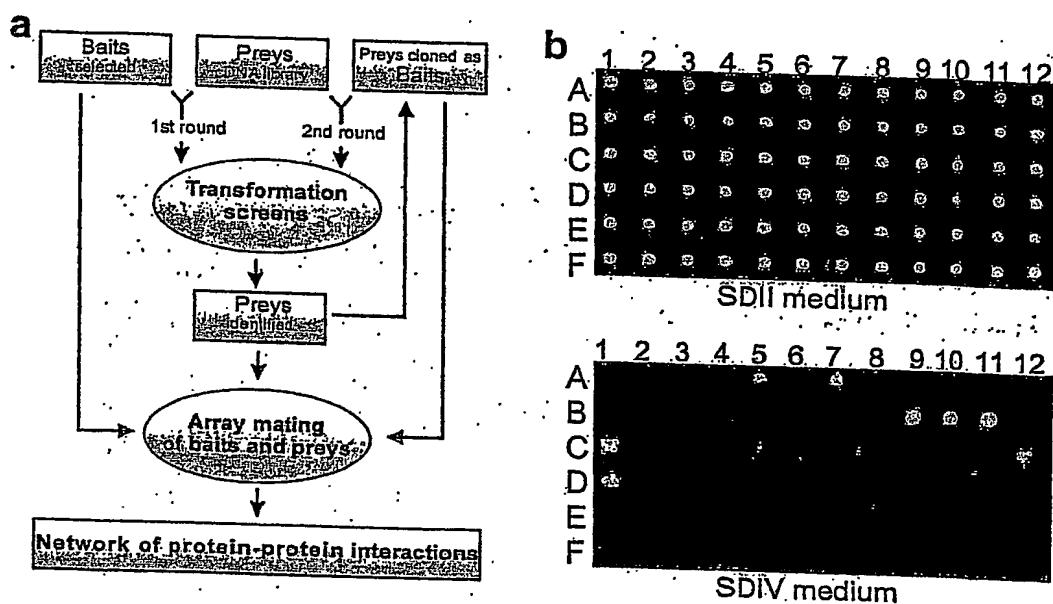


Figure 1

BEST AVAILABLE COPY

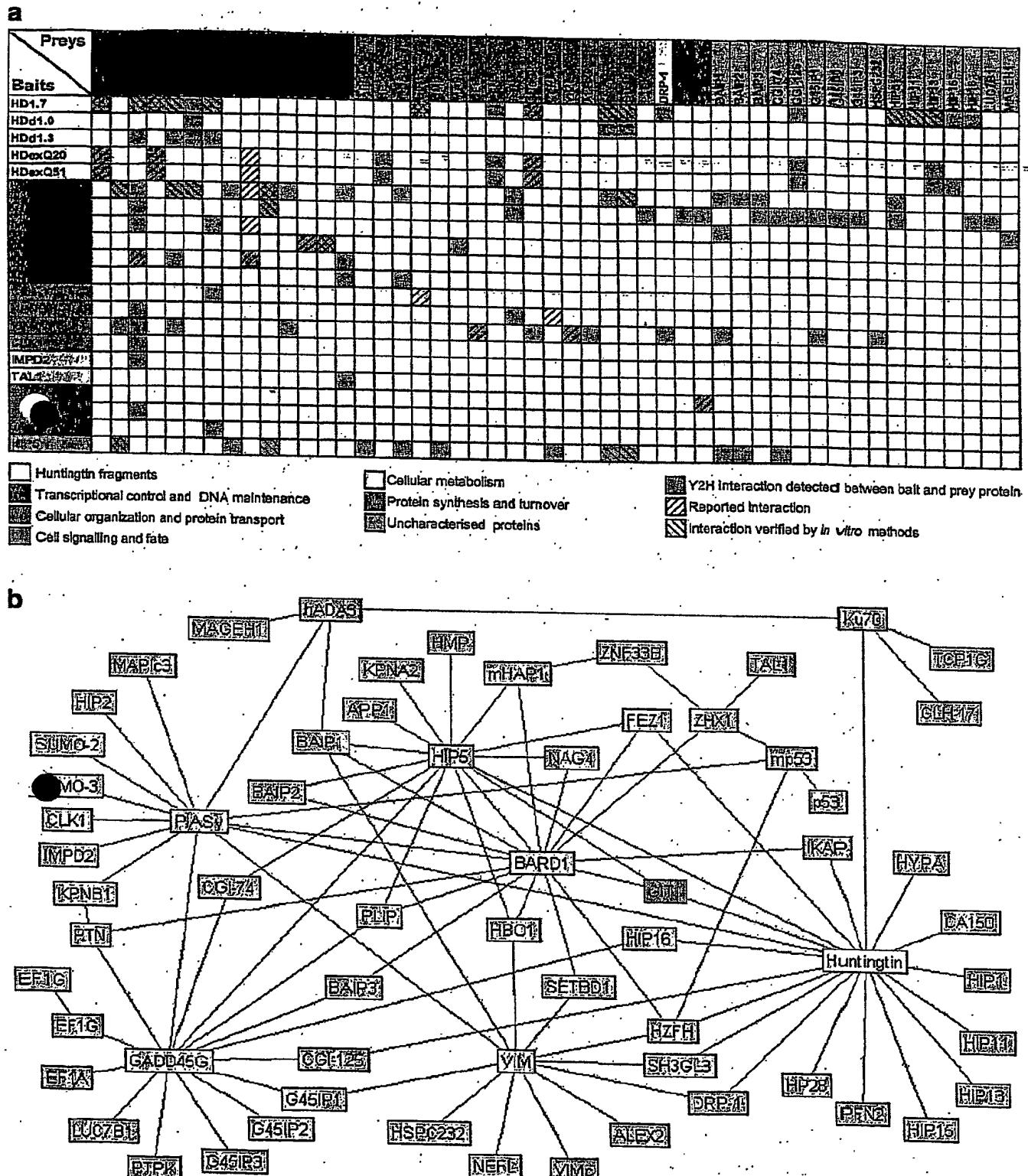


Figure 2

BEST AVAILABLE COPY

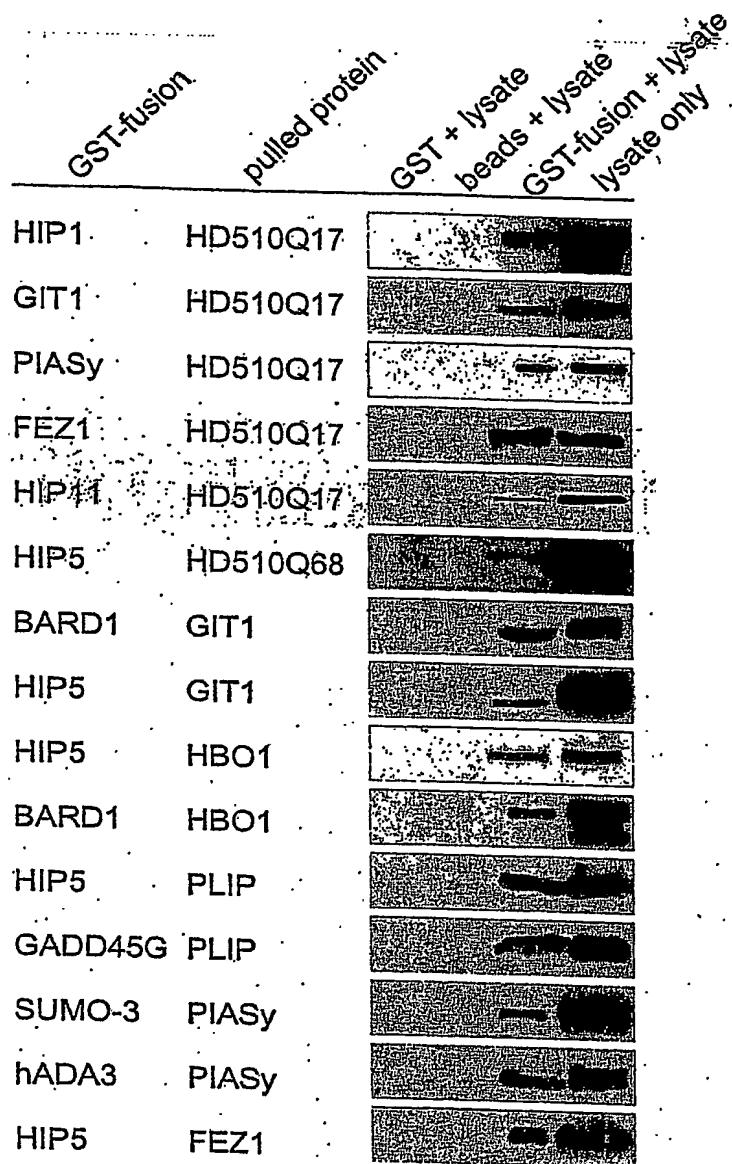


Figure 3

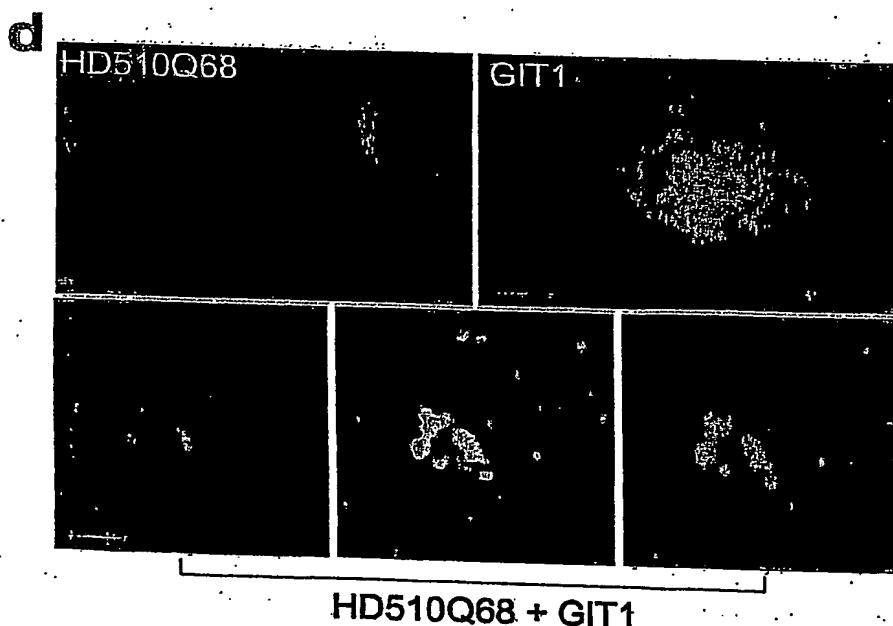
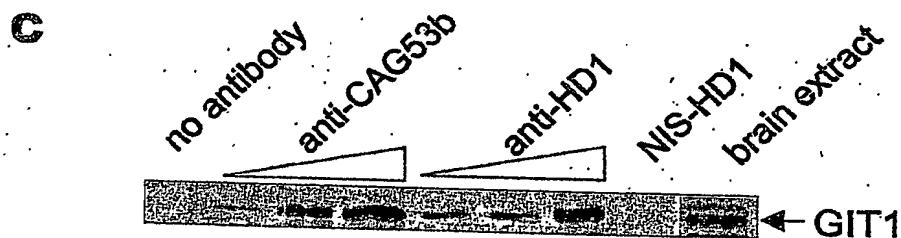
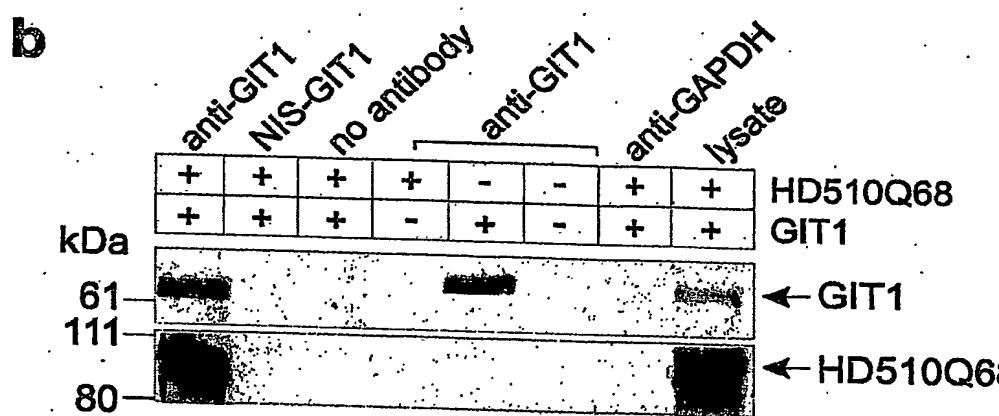
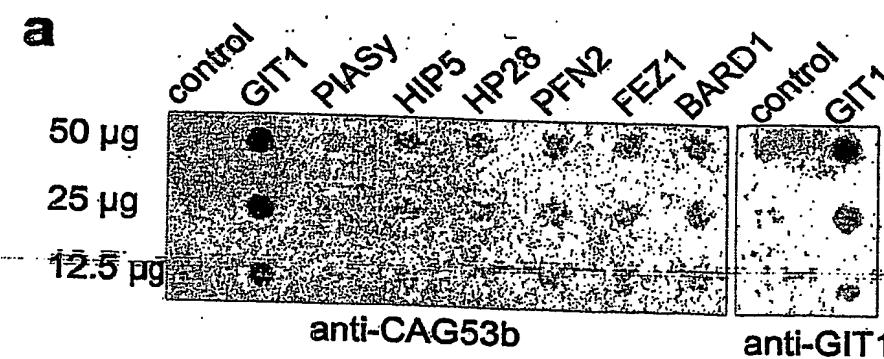
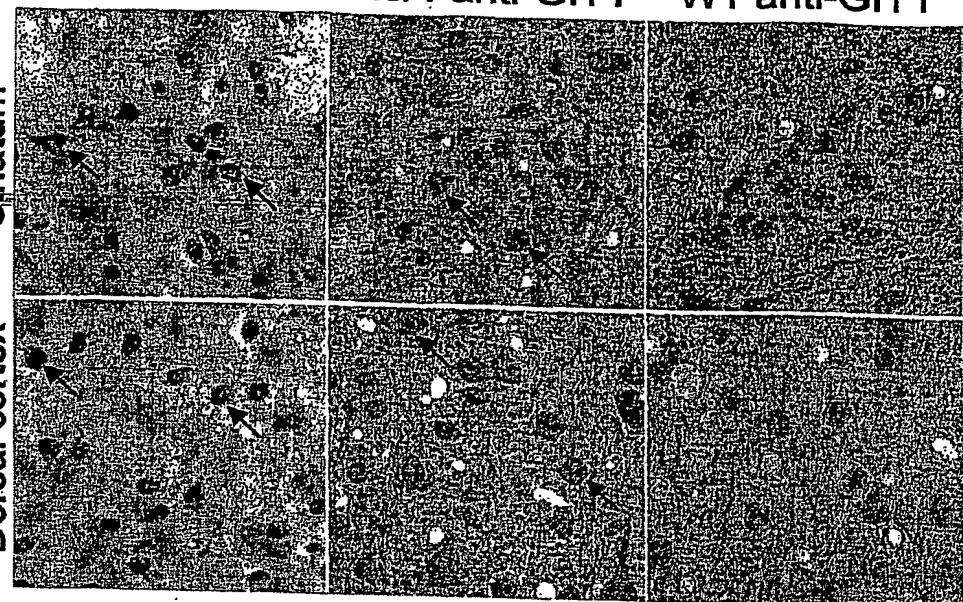


Figure-4

a R6/1 anti-htt R6/1 anti-GIT1 WT anti-GIT1

Striatum

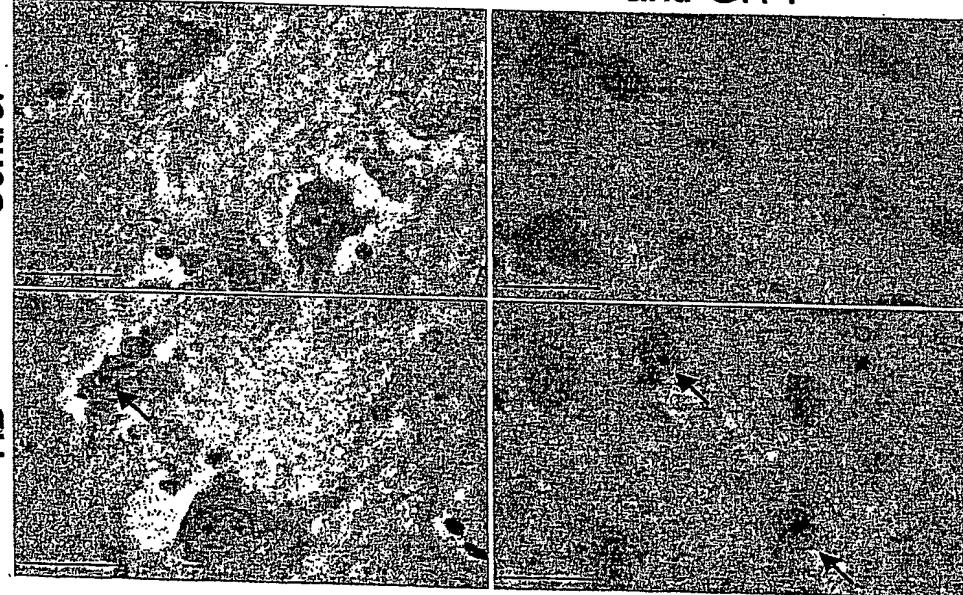


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b anti-htt anti-GIT1

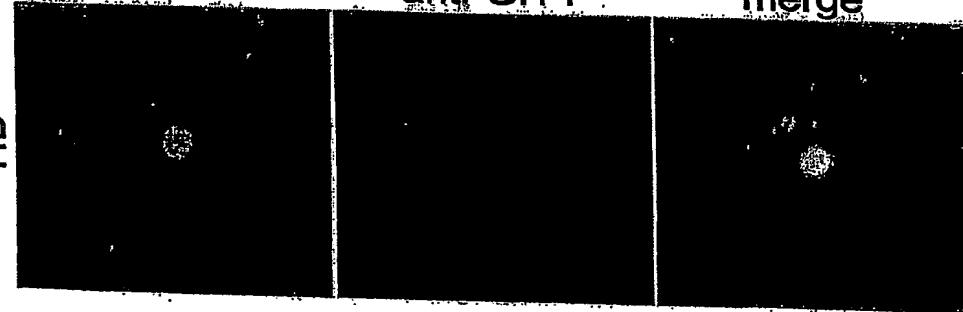
Control

HD



c anti-htt anti-GIT1 merge

HD



>ALEX2
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 ATPGAHTGAIPKATSATGAVPKGGKGVTRSRNGGKGKSKVEVDELMGFRPGDGAAGAAA
 ANGQOFLAEVPDSEEGESGWTDTESDSDSEPETQRGRGRPVAMQKRPPYEIDEILGVRDLRK
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 EDYENQCRQVVMNKVMBDTMASNINSAVQVVGKFLTNMTITNDYQHLLVNSIANFFRILSQGGG
 KIKVEILKILSNFAENPDMLKKLSTQVPAFSSLVNSYVESEILINALTLFEIYDNLRAEVFNY
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 >APP1
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 GFLRAKMDLEERRMRQINEVMREWAMADNQSKNLPKADROALNEHFQSILOQTLERQVSGERQRLVE
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 >BAIP1
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 >BAIP2
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 >BAIP3
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 WAHSRAALDRLEKLLRCRCTNILREPVCGLGGCEHIFCSNCVSDCIGTGCPCVYTPAWIQLDKINR
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 VTPEKVKNYLTSKKSLPLENNKGRRGHHNRLSSPISKRCRTSILSTSGDFVKQTVPSENIPLPECS
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 >CA150
 QQFIPGPLKILVWPCCLFQSAPTTQDQTPSSAVSVATPTSVSTPAPTATPVQTVQPHPQTLPPA
 VPHSVQPTTAIPAFPPVMPPFRVPLPGMPIPLPGVLPGMAPPIVPMIHPQVAAIASPATLAGAT
 AVSEWTEYKTADGKTYYYNNRTLESTWEKPKQELKEKEKLEEKIKEPIKEPSEEPLPMETEEEDPKE
 EPIKEIKEPKEEEMTEEEKAQAKPVATAPAPIPGTPWCVWTGDERVFFYNPTTRLSMWDRPDDL
 IGRADVDKIIQEPFHKKGMEELKKLRHPTPTMLSIQKWQFSMSAIKEEQLMEEINEDEPVKAKKR
 K

Figure 6

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>CGI-125
FDASARNFARVSGLLLQAGGVLVSSFVMAAVAMETDDAGNRLRFQLELEFVQCLANPNYLNFLA
QRGYFKDKAFVNLYKLLYWKDPEYAKYLKYPQCLHMLELLQYEHFRKELVNAQCAKFIDEQQILH
WQHYBSRKRMRLQQAIAEQQQONNTSGK

>CGI-74

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GEELKKRVAEKQEKRNQERLKRREEREREREREKLRRSRSHSKNPKR
>CLH-17

SCNR-17

MAQILPIRFQEHLQLQNLGINPANIGFSTLTMESDKFICIREKVGEQAQVVIIDMNDPSNPIRRPI
SADSAIMNPASKVIALKAGKTLQIENIEMSKMKAHTMTDDVTFWKWIISLNTVALVTDNAVYHWSM
EGESQPVKMFDRHSSLAGCQIINYRTDAKQKWLLTGISAQQNRVVGAMQLYSVDRKVSQPIEGHA
ASFAQFKMEGNAESTLFCFAVRGQAGGKLHIIIEVGTPTGNQPFPKKAVDVFPEAQNDFPVAM
QISEKHDVVFLITKYGYIHLYDLET

>CLK1

DAWVLEHLNTTDPNSTFR^CVQML^EWF^HHHG^HI^CIVF^LLL^GL^STYDF^IK^ENGFLP^FR^LD^HIR^KMA^YQ^ICKSVN^FLHS^NKL^LT^HDL^KPEN^ILF^VQ^SD^YTE^AYN^PK^IK^RDER^TL^IN^PD^IK^VV^DFG^SAT^YD^IE^HH^S
TLV^STR^HYRAPE^VI^LAL^GWS^QPC^DV^WS^IG^CIL^EYY^IL^GFT^VF^PTH^DS^KE^HLAMMER^RIL^GPL^KH^MI^QK^TR^KR^KY^FH^HD^RL^DW^DE^HS^SAG^RY^VS^RR^CK^PL^KE^FM^LS^QD^VE^HER^LF^DL^IQ^KM^LE^YD^PA^KR^IT^LR^EALK^HP^FF^DLL^KK^SI¹

>DRP-1

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IWDPDKLKTITAKSHKSAVEYNIFEGMECHGSPVVISQGKIVFEDGNINVNGMGRFIPRKAFPE
HLYQRVKIRNKVFGLQGVSRGMYDGPVYEVPATPKYATPAPSAKSSPSKHQPPPIRNLHQSNFSL
GAQIDDDNNPRTGHRIVAPPGRSNITSLG

>EF1A

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VRDMRQTVAVGVIKAVDKKAAGAGKVTKSQAKAQQAKAK
-PPIG-(bait)

>EF1G(bait)

AAGTLYTYPENWRAFKALIAAQYSGAQVRVL\$APPFHFGQTNRTPFELRKFPAGKVPAGFEGDDGF
CVFESNAIAYYVSNEELRGSTPEAAAQVWQWSFADSDIVPPASTWVFPTLGIHMHNKQATENAKE
EVRRILGLLDAYLKTRFLVGERVTLADITVVCTLLWLYKQVLEPSFRQAFPNTNRWFLTCINQPQ
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TWRKLDPGSEETQTLVREYFSWEGAFQHVGKAFNQGKIFK
>EE1G (prev)

PEET (Pey)
AAGTLVTVBEM

AAGILITIYPENWRALKALIAAQYSGAQVRVLSAPPFHFGQTNRTPFELRKFPAGKVPAGFEGDDGF
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LTQTFMSCNLITGMFQRILDKLRKNAFASVILFGTNNSSSIISGVWVFRGQELAFPLSPDWQVDYESY
TWRKLDPGSEETQTLVREYFSWEGAFQHVGKAFNQGKIFK
- EKZ1

SPEZI
SMEGT

GNCSDTEIHEKEEEFNEKSENDSGINEEPLLADQVIEETEMMQNSPDPEEEEVLEEDGGET
SSQADSVLLOEMQALTQTFNNNWSYEGLRHMSGSELTELLDQVEGAIRDFSEELVQQLARDELEF
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Figure 6 (continued)

>G45IP1

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 KKLQMRKAYVVKTTENKDHYVTKKKLVTEHKDTEDFRQDFHSEMSGFCKAALNTSAGNSNPYLPYS
 CELPLCYFSSKCMCSSLGGPVDRAPDSSKDGRNHHKTMGHYNHNDSLRKTQINSLKNSVACPGIAQKA
 ITSSEAVDRFMPRTTOLQERKRRREDDRKLGTFLOTNPTGNEIMIGPLPDISKVDMHDDSI_NTTA
 NITRHKLKEVTSVPKPPEDKPEDVHTSHPLKQRRRI

>G45IP2

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 GCFCAAGCSRQIGFSFVRPKLCAFSGLYYCDICHQDDASVIRARIHWNWLTKRPICRQALKFLTQI
 RAQPLINLQMVNASLYEHVERMHILIGRRREQLKLLGDYLGLCRSGALKELSKRLNHRNYLESPHR
 FSVADLQQIADGVYEGFLKALIEFASQHVVHCDLCTQRGFICQICQHHDIIFPFEEFTTVRCAECK
 TVFHQSCQAVVKKGCPRCARRRKYQEONIFA

>G45IP3

PNRGPPLSPPNDLRPSHVISLPLHNAPHTRPTNQHTNHIPMMARCNTRKHIPRPPHTCPKRP5IRD
 NPIYYLRSFFLRRIFLSLLPLQPSPYPPIRRALAPNRHHPAKSPRSPTPKHIRITRIRSINHLSSP
 >GADD45G

GAGAEGGLECGWSWGAKGVCRWPGGLSPPRPPAGSRSLRWLLRRMQGAGKALHELLLSAQRQGCLT
 AGVYESAKVLMVDPDNVTFCVLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGVDVQRLAAIVG
 AGEEAGAPGDLHICLISNPNEADWKDPALEKLSLFCEESRSVNDWVPSITLPE

>GIJ1

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 RSQSDLDDQHDYDSVASDEDTDQEPLRSTGATRSNRARSMDSSDLSDGAVTLQEYLELKKALATSE
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 RQAFSMYEPGSALKPFGPPGDELTTRLQPFHSTELEDDAIYSVHVPAGLYRIRKGVSASAVPFTP
 SSPLLSCSQEGRHTSKLSRHGSADSDYENTQSGDPLLGLEGKRFLELGKEEDFHPELESLDGDL
 DPGLPSTEDVILKTEQVTKNIQELLRAAQEFKHDHFVPCSEKIHLAVTEMASLFPKRPALEPVRSS
 LRLLNASAYRLQSECRKIVPPEPGAPVDFQLLTQQVIQAYDIAKAAKQLVTITREKKQ

>hADA3

KDVLALLKKSEAQHEQPEDGCPFGALTQRLLQALVEENIISPMEDSPIPDMSGKESGADGAS TSPR
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 LLRLAKEEVSRQELRQVRMADNEVMDAFRKIMAARQKKRTPTKKEKDQAWKTLKERESILKLLDG
 >HB01

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 IYCQNLCLLAKLFLDHKTLYYDVEPFLFYVMTEADNTGCHLIGYFSKEKNSFLNVNVSCILTMPQY
 MRQGYGKMLIDFSYLLSKVEEKVGS PERPLSDLGLISYRSYWKEVLLRYLHNFGKEISIKEISQE
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Figure 6 (continued)

Figure 6 (continued)

>HIP16

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 TTPKVVTKPGHIINPIKAEDVGYRSSSRDLSVIQRNPKRITTRHKKQLKKCSVD

>HIP2

MANIAVQRIKREFKEVLKSEETSKNQIKVDLVDENFTELRGEIAGPPDTPYEGGRYQLEIKIPETY
 EENEPKAVRFTTCWIDPNISSVIGAICEDTLDQWAAMTIRTVLLSLOALLAAEPDDPQDAVAN
 QYKQNPEMFKOTARLWAHIVYAGAPVSSPEYTKKIELCAMGFDRNAVIVALSSKSWDVTATELL
 SNX

>HIP5 (bait)

FLKSLILKESKYEHGYLKALIINQSFKFGNQKAAIRDSIELTKEKGAEIPKTIKKLRWFDETSNI
 ENNAENSHSLKNKTGTTQQHSQQFHIQSGAGSNIIISVSTCAVNSADTKKSREDSISENVTTLGGSG
 ADHMPNCFIPSGYNFAKHAWPASKKEESKIPVHDDSKTKQGKQRGRAKIIRKPGSAKVQSGFIC
 TNRKGAVIQPQSASKVNIFTQAQGKLIIPCPPPQSTSNIIRSGKNIQVSQCQPVTPENPONIITHNS
 FNSKHVLPTEHSLNQWNQESSSPLSNACSDLVTVPISLPSYCSECQTFAKINHSNGTQAVARQDA
 TLYCTQRSPVCEESYPSVTLRTAEEESVPLWKRGPNVLHQNKATGSTMRRKRIAETKRRNILEQ
 KRQNPQSGVGQKYSEQINNFGQSVLLSSEPKQTTRGTSYIEEVSDSTSEFLMAENLVKASVPEDEI
 LTVLNSKQIQKSNLPLNKTQOFNICTLSAEEQKILESLNLDLNERLHYIQESICKNPSIKNTLQIIP
 LLEKREDRTSSCRDKR

>HIP5 (prey)

FLKSLILKESKYEHGYLKALIINQSFKFGNQKAAIRDSIELTKEKGAEIPKTIKKLRWFDETSNI
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 ADHMPNCFIPSGYNFAKHAWPASKKEESKIPVHDDSKTKQGKQRGRAKIIRKPGSAKVQSGFIC
 TNRKGAVIQPQSASKVNIFTQAQGKLIIPCPPPQSTSNIIRSGKNIQVSQCQPVTPENPONIITHNS
 FNSKHVLPTEHSLNQWNQESSSPLSNACSDLVTVPISLPSYCSECQTFAKINHSNGTQAVARQDA
 TLYCTQRSPVCEESYPSVTLRTAEEESVPLWKRGPNVLHQNKATGSTMRRKRIAETKRRNILEQ
 KRQNPQSGVGQKYSEQINNFGQSVLLSSEPKQTTRGTSYIEEVSDSTSEFLMAENLVKASVPEDEI
 LTVLNSKQIQKSNLPLNKTQOFNICTLSAEEQKILESLNLDLNERLHYIQESICKNPSIKNTLQIIP
 LLEKREDRTSSCRDKR

>HMP

QBQVKIESLAKSLEDALRQTASVTLQAIAAQNAAVQAVNAHSNILKAAMDNSEIAGEKKSAQWRTV
 EGALKERRKAVDEAADALLKAKEELEKMKSVIENAKKKEVAGAKPHITAAEGKLHNMIVDLDNVVK
 KVQAAQSEAKVVSQYHELVVQARDDFKRELDSTPVELPGWKGMSVSDLADKLSTDDLNSLIAHAH
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 ENEMRTQLRROAAHTDHLRDVLRVQEQLSEFQNLSEKLSSEQELQFRRLSQEQVDNFTLDINT
 AYARLRGIEQAVQSHAVAEEEARKAHQLWLVEALKYSMKTSSAETPTIPLGSAVEAIKANCSDNE
 FTQALTAIIPPESLTRGVYSEETLRARFYAVQKLARRVAMIDETRNSLYQYFLSYLQSLLLFPQQ
 LKPPPELCPEDINTFKLISYASCYIEHGDILELAAKFVNQLKGESRRVAQDWLKEARMTLETQIIVE
 ILTAYASAVGIGITQVQPE

>HP28

PPADSLIKYDTPVLVSRNTEKRSRKARLLKVSPQQPGPSGSAPQPPKTKLPSTPCVDPDKQAEII
 LNAILPPREWVETQLWIQQVSSTPSTRMDVVHLQEQQLDLKLIQQRQARETGICPVRRELYSQCFDE
 LIREVTINCAERGLLLLRLRDEIRMTIAAYQTLYESSVAFGMRKALQAEQGKSDMERKIAELETEK
 RDLERQVNEQKAKCEATEKRESERRQVEEKKHNEEIQFLKRTNQQLKAQLEGIIAPKK

>HSPC232

ERRADGCIYGVSRARVAYRDEMSEGRYERYIIPRERAPPRSHPSDESGYRWRDDHSASRQP
 EYRDMRDGFRRKSFYSSHYARERSPYKRDNTFFRESPVGRKDSPHSRGSSVSSRSYSPERSKSYS
 FHQSQHRNKERPVQSLKTSRDTSPSSGSAVSSSKVLDKPRLTEKELEAAASKWAAEKLEKSDESN
 LPHEISEYEAGSTAPLFTDQPEEPESNTTHGIELFEDSQLTTRSKAIASKTKEIEQVYRQDCETFGM
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Figure 6 (continued)

>HYPA

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 QSTWEKPDDLKTPAEQLSKCPWKEYKSDSGKPYYNSQTKESRWAKPKELEDLEGYQNTIVAGSL
 ITKSMLHAMIKAEESSKQEECTTSTAPVPTTEIPTTMSTMAAAEAAAAVVAAAAAAAANA
 NASTSASNTVSGTVPVVEPEVTSIVATVVDNENTYTISTEEQALTSRAIQDOSVIEVSNEGH
 TSQETVADFTPKEEEEESQAKTYTWNTEKEAKQAFKELIKEKRVPSNASWEQAMKMIINDPRY
 SALAKLSEKKQAFNAYKVQAKKEKKKKKK

>HZFH

HARFAAECLAESHQHLSKESLAGNKPANAVLHKVNLQLEELLSDMKADVTRLPATLSRIPPIAAR
 LQMSERSILSRLASKGTPEPHPTPAYPPGPYATPPGYGAFAFSAPVGALAAAGANYSQMPAGSFITA
 ATNGPPVLVKEKEKEMVGALVSDGLDRKEPRAGEVICIDD

>IKAP

LKEGSPLEDLALLEALSEVVQNTENLKDEVYHILKVLFLFEFDEQGRELQKAFEDTLQLMERSLPE
 IWTLTYQONSATPVLGPNSTANSIMASYQQQKTSVPVLDALFIPPKINRRTQWKLSLDD

>IMPD2

DFLILPGYIDFTADQVDLTSALTKKITLKTPLVSSPMVTVEAGMAIAMALTGGIGFIHHNCTPEF
 QANEVRKVKKYEQGFIIDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLVGIISSRDIDF
 LKEEEHDCFLEIMTKREDLVAAPAGITLKEANEILQRSKKGKLPIVNEDDELVAI LARTDLKKNR
 DYPLASKDAKKQLLCGAAIGTHEDDKYRLDILLAQAGVDVVVLDSQGNSIFQINMIKYIKDKYPNL
 QVIGGNVVTAAQAKNLIDAGVDALRVMGSGSICITQEVLACGRPQATAVYKVSEYARRFGVPVIA
 DGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKRYGMGLDAMDKHLSSQNR
 YFSEADKIKVQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVRAMMYSGELKEKRTS
 SAQVEGGVHSLHSYEKRLF

>KPNA2

AWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHAISEQAVWALGNILAGDGSVFRDLVIKYGAV
 DPLLALLAVPDMSLACGYLRNLTWTLNSNLCRNKNPAPPIDAVEQILPTLVRLLHHDDPEVLA
 WAIISYLTDPGPNERIGMVVKITGVVPQLVKLLGASELPIVTALRAGNIVTGTDEQTQVVIDAGALA
 VFPSSLTNPKTNIQKEATWTMSNITAGRQDQIQQVNVHGLVPFLVSLSKADFKTQKEAVWAINTY
 TSGGTVEQIVYLVHCGITEPLMNLLTAKDTKIIILVILDAISNIFQAAEKLGETEKL SIMIEECGGL
 DKIEALQNHENESVYKASLSLIEKYFSVEEEEEDQNVVPETTSEGYTFQVQDGAPGTFNF

>KPNB1

LAAVGLVGDLCRALQSNITIPFCDEVMQLLLENLGNEVHRSVVKPQILSVFGDIALAIGGEFKYLE
 VVLNTLQQASQAQVDKSDYDMVDYLNELRESCLEAYTGIVQGLKGDOENVHPDVMLVQPRVEFILS
 FIDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVLKLVEARPMIHELLTEGRRSKTNKAKTLATWA
 TKELRKLKNQA

>Ku70

KTRTFNTSTGGLLLPSDTKRSQIYGSRQIILEKEETEELKRFDDPGIMLMGFKPLVLLKKHYLRP
 SLFVYPEESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQKIQVT
 GFQLVFLPFADDKRKMPTEKIMATPEQVGKMKAIIVEKLRFTYRSDSFENPVLQHQFRNLEALALD
 LMEPEQAVDLTLPKVEAMNKRGLGSVDEFKELVYPPDYNPEGKVTKRKHDNEGSGSKRPKVEYSE
 ELKTHISKGTLGKFTVPMLEACRAYGLKSGLKKQELLEALTKHQD

>LUC7B1

VDAAVDAAAVSAKAEKVHELNEKIGKLLAKAEQLGAEGNVDESQKILMEVEKVRACKKEAEEYR
 NSMPASSFQQQKLRVCEVCSAYLGLHDNDRRLADHFGGKLHLGFIQIREKLDQLRKTVAEKQEKR
 QDRLRRREEREREERLSRRSGSRTRDRRRRSRSRSTSERRKLSRSRSRDRHRRHRSRS
 RSHSRGHRRASRDRSAKYKFSRERASREESWESGRSERGPPDWRLESSNGKMAARRSEEKEAGEI

Figure 6 (continued)

>MAGEH1
 ASFPTAVSFEPPLAGDMRGRKSRRRNARAEEENRNNRKIQASEASETPMAASVVASTPEDDL
 PEEDPSTPEEASTTPEEASSTAQAQKPSVRSNFQGTKKSLMSILALIFIMGNSAKEALVWKVLG
 KLGMQPGRQHSIFGDPKKIVTEFVRRGILITKPVPRSSPVEYEFFWGPRAHVESSKLKVMHFVAR
 VRNRC8KDWPONYDWDSSDAEVEAILNSGARGYSAP
 >MAP11c3
 QRR9TADRCKEVQGTRDQHPSKTPVITERYKGEKOLPVLDKTKFLVPDFVNMSELVKIIIRRLQLN
 PTQAFFLIVNQHSMVSVSTPIADIYEQEKDQDFLYMVYASQETFGF
 >mHAP1
 PKEQVQSGAGDGTGSGDPAAGPTTQPAVGPAPEPSAEPKPAPAQGTGSGQKSGSRTKTGSFCRSM
 IIGDSDAPWTRYVFQGPGPRATGLGTGKAEGIWKTAAIGQSLVKQNSVLMEEENNLETMLGSAREEILHLRK
 PPPTKKITTEDDVKVMYLLEEKERDLNTAARIGQSLVKQNSVLMEEENNLETMLGSAREEILHLRK
 QVNLRDDLLQLYSDSDDDDDEEDEDEEEGEEREQQRDQDQHDPYGAQPKPHPKAETAHRCPO
 LETLQQKLRLLEENDHLREASHLDNLEDEEQMLILECVEQFSEASQMAELSEVVLVRLEGYER
 QKETIQLQAEITKLOQRCQSYGAQTEKLOQMLASEKGHSRAGSYMDYGSRPRDRQEDGKS
 HRQRSSMPAGSVTHYGYSVPLDALPSFETLAELRTSLRKFITDPAYFMERRDTHCREGRKKEQR
 AMPPPPAX
 >mp53
 VTETPGVAPAPATPWPLSSFVPSQKTYQGNYGPHLGFLQSGTAKSVMCTYSPPLINKLFCQLAKTC
 PVQLWVBATPPAGSRVARAMAIYKKSQHMTEVVRCPHHERCSDGGLAPPQHLIRVEGNLYPEYLE
 DRQTFRHSVVVPYEPPEAGSEYTTIHYKYMNCNSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVR
 VCACPGRDRRTTEENFRKKEVLCPELPPGSAKRALPTCTSAPPQKKPLDGEYFTLKIRGRKRFE
 MFRELINEALELKDAHATEESGDSRAHSYLLKKGQSTSRRHKTMVKVGPDS
 >NAG4
 RDRVNEAEKDLQCHAPVRLDLPPEKPLTSIYQEEVEQTPQLEALNQLMRQLQRKDPSSAFFSFP
 VTDFIAPGYSMIKHPMDSTMKEKIKNNDYQSIIEELKDNFKLMLCTNAMITYNKPETIYYKA
 HSGMKILSQERIQSLKQSIDFMADLQKTRKQKDGTDSQSGEDGGCWQREREDSGDABAHAFKSPS
 KENKKDKDMLEDKFKNLNEREQEQLDRIVKESGGKLTRRLVNSQCEFERRKPDGTTLGLLHPV
 DPIVGEPGYCPVRLGMTTGRILQSGVNTLQGFKEDKRNKVTPVLYLNYGPSSYAFHYDSTFANISK
 DDSDLIYSTYGEDSDLPSDFSIEFLATCQDVYPMADSLLDVLTKGGHSRTLQEMEMSLPEDEGH
 TRTLDTAKEMITEVEPPGRILDSSTQDRLIALKAVTNFGVPVEFDSEEEAIQKKLDETTRLLRE
 LQEAAQNERLSTRPPPNNMICLLGPGSYREMHLAEQVTNNLKELAQQTFGDIVSTYGVRKAMGSI
 PSMENINFVDLTEDTEEPKKTDAECGPAGS
 >NEFL
 LSPLSSLSGLPPPRAJEEPAATMSSFSYEPYISTSYKRRYVETPRVHISSVRSGYSTARSAYSSY
 SAPVSSSLSVRRSYSSSSGSLMPSLENLDLSQVAASIENDLSQKTSITQKEAQLQDLNDRFASFIERVH
 ELEQQNKVLEAELLVLRQKHSEPSRFRALYEQEIRDLRLAAEDATNEKQALQGEREGLEETLRNLQ
 ARYEEEVLSREDAEGRILMEARKEADEAALARAELEKRIDSLLMDEISFLKKVHEEHLAELQAOIQYA
 QISVEMDVTKPDLSSAALKDIRAQYEKLAANKMQNAEWFKSRTVLTESAACKNTDAVRAAKDEVSE
 SRLLKAKTLEIEACRGMNEALEKQLQELEDKQNADISAMQDTINKLENLRTTKSEMARYLKEYQ
 DLLNVKMDIEIAAYRKILLEGRETLSFTSVGSITSGYQSQSQVGRSAYGGLQTSYLMSTRSF
 PSYYTSHVQEEQIEVEETIEAAKAEAKDEPPSEGEAEEEEKKEEEAEEEEAAKEESEEEA
 KEEEEE
 >p53
 MEEPQSDPSVEPPLSQETFSDLWKLPPENNVLSPLSQAMDDMLSPDDIEQWFTEDPGPDEAPRM
 PEAAPPVAPAPAAPTPAAPAPAPSWPLSSVPSQKTYQGSYFRLGFLHSQGTAKSVTCTYSPLN
 MFCQLAKTCVQLWVDSTPPPGRVRAAMAIYKQSQHMTEVVRCPHHERCSDSDGLAPPQHLIRVE
 GNLRVEYLLDRNTFRHSVVVPYEPPEVGSDCTTIHYNMNCNSCMGGMNRRPILTIITLEDSSGN
 LGRNSFEVRVCACPGDRRTTEENLRKKGEPHELPGSTKRALPNNTSSSPQPKKKPLDGEYFTL
 QIRGRERFEMFRELINEALELKDAQAGKEPGGSRAHSHLKSKKGQSTSRRHKKLMFKTEGPDS

Figure 6 (continued)

>PFN2

APRRPRCSAKGSKMAGWQSYVDNLMCDGCCQEAIIVGYCDAKYVWAATAGGVFQSITPIEIDMIVG
KDREGFFTNGLTLGAKKCSVIRDSLVDGDCTMDIRTKSQGGEPTYNVAVGRAGRVLVFVMGKEGV
HGGGLNKKAYSMAKYLRDSGF

>PIASy (bait)

LVEAKNMVMSFRVSDLQMLLGFGVGRSKSGLKHELVTRALQLVQFDCSPELFKKIKELEYETRYAKN
SEPAPOPHRPLDPLTMHSTYDRAGAVPRTPLAGPNIDYPVLYGKYLNGLGRPAKTLKPEVRLVKL
PFFNMLDELLKPTELVQPNNEKLQESP C I F A L T P R Q V E L I R N S R E L Q P G V K A V Q V V L R I C Y S D T S C
PQEDQYPPNIAVKVNHSYCSVPGGYPSNKGVEPKRPCRPINLTHLMLYSSATNRITVTWGNYGKS
YSVALYLVRLTSSELLQRLKTIGVKHPELCKALVKEKLRLDPDSEIATTGVRVSLICPLVKMRLS
VPCRAETCAHLQCFDAVFYLQMNEKKPTWMCVCDKPAPYDQLIIDGILSKILSECEADEIEYLV
DGSWCPIRAEKERSCSPOGAILVLGPSDANGLLPAPS VNGSGALGSTGGGPVGSMENGKPGADVV
DLTLDSSEDEEEEEEDEDEEGPRPKRRCPFQKGLVPAC

>PIASy (prey)

LVEAKNMVMSFRVSDLQMLLGFGVGRSKSGLKHELVTRALQLVQFDCSPELFKKIKELEYETRYAKN
SEPAPOPHRPLDPLTMHSTYDRAGAVPRTPLAGPNIDYPVLYGKYLNGLGRPAKTLKPEVRLVKL
PFFNMLDELLKPTELVQPNNEKLQESP C I F A L T P R Q V E L I R N S R E L Q P G V K A V Q V V L R I C Y S D T S C
PQEDQYPPNIAVKVNHSYCSVPGGYPSNKGVEPKRPCRPINLTHLMLYSSATNRITVTWGNYGKS
YSVALYLVRLTSSELLQRLKTIGVKHPELCKALVKEKLRLDPDSEIATTGVRVSLICPLVKMRLS
VPCRAETCAHLQCFDAVFYLQMNEKKPTWMCVCDKPAPYDQLIIDGILSKILSECEADEIEYLV
DGSWCPIRAEKERSCSPOGAILVLGPSDANGLLPAPS VNGSGALGSTGGGPVGSMENGKPGADVV
DLTLDSSEDEEEEEEDEDEEGPRPKRRCPFQKGLVPAC

>PLIP

GEIIEGCRLPVLRNQDNEDEWPLAEILSVKDISGRKLIFYVHYIDFNKRLDEWVTHELDLKKIQF
PKKEAKTPTKNGLPGSRPGSPEREVKRKVEVVSPATPVPSETAPASVFPQNGAARRAVAAQPGRKR
KSNCLGTDQSQDSSDGIAPSAPMTGSLVSDRSHDDIVTRMKNIECIELGRHRLKPWYFSPYPQEL
TTLFVLYLCEFCLKYGRSLKCLQRHLTKCDLRHPPGNEIYRKGTISFFEIDGRKNKSYSQNLCLLA
KCFLDHKTLYYDTDPFLFYVMTEYDCKGFHIVGYFSKEESTEDYNVACILTLPFYQRRGYGKLLI
EFSYELSKVEGKTGTPEKPLSDLGLLSYRSYWSQITLEILMGLKSESGERPQITINEISEITSIKK
EDVISTLQYLNLLINYYKGQVILTLSEDIVDGHERAMLKRLRIDSKCLHFTPDKWSKRGKW
>PTN

LSQRQDQVPRLPVQKSROESPRAEENPKWREGKKETSESSVQKAGRAAAQAGAAASRVPGLSGSN
LAPCNKGRLSAREDVSNSKMQAQQYQQQRRKFAAFLAFIFILA AVDTAEAGKKEKPEKKVKKSDC
GEWQWSVCVPTSGDCGLTREGITRTGAECQTMKTQRCKIPCNWKKQFGAECKYQFQAWGECDLNT
ALKTRGSLKRALHNAECQKTVTJSKPCGKLTKPKPQAESKKKKEGKKQEKMLD
>PTPK

SNYINAALMDSYRQPAAFIVTQYPLPNTVKDFWRLVYDYGCTSIVMLNEVDLSQGCPQYWPEEGML
RYCPIQECMCSMDCDVINRIFRICNLTRPQEGYLMVQQFOYLGWASHREVPGSKRSFLKLILQV
EKWQECEEGEGRTIHCLNGGGRSGMFCAIGIVVEMVKRQNVDVFHAVKTLRNSKPNMVEAPEQ
YRFCYDVALEYLESS

>SETBD1

KASTSGLGIKDEGDIKQAKKEDTDDRNKMSVVTTESSRNYGYNPSPVKPEGLRRPPSKTSMHQSRL
MASAQSNPDDVLTLSSTSESEGESGTSRKPTAGQTSATAVDSDDIQTISSGSEGDDFEDKKNMGTGP
MKRQVAVKSTRGFALKSTHGIAIKSTNMASVDKGESAPVRKNTRQFYDGEESCYIIDAKLEGNLGR
YLNHSCSPNLVQNVFVDTHDLRFPWV AFFASKRIRAGTELWDYNYEVGSVEGKELLCCGAIEC
RGRLL

Figure 6 (continued)

>SH3 GL3

VÄGLKKQPHKÄSÖLFSEKISGAEGTKLDDEFLDMERKIDVINKVVAEILSKTEYLQPNPÄYRAKL
 GMLNTVSKIRGQVTTGYPQTEGILLGDCMLKYGKELGEDSTFGNALIEVGESMKLMAEVKDSLIDIN
 VKÖTFIDPLQLLQDKDLKEIGHHLKKLEGRRLDYKKRVCKİPDEEVROAVEKFEESKELAERS
 MFNFLENDVEQVSQLAVFIEAALDYHRQSTEILQELQSKLOMRSAAASVPRREYKPRPVKRSSSE
~~ENGVSTTSEVAKTTCGSNIPMBQRCGPGLVBDPBMQGBLGPIDTITLNGQDENDWYEGMHEHESG~~
 FFPINYVEVIVPLPQ

>SUMÖ-2

RPRÄQLRRESGGAESVTRPLRAASPAFPRAARAAMSEEKPKEGVKTENDHINLKVÄGQDGSVVQF
 KIKRHTPLSKLMKAYCERQGLSMRQIRFRFDGQPINETDTPÄQLEMEDEDTIDVFQQQTGGVPESS
 LAGHSF

>SUMÖ-3

PSSSTAAÄSFPFCRSWCCLCAREVRTWYLFCEAAAEETPALAMADEKPKEGVKTENNDHINLKVÄGQD
 GSVVQFKIKRHTPLSKLMKAYCERQGLSMRQIRFRFDGQPINETDTPÄQLEMEDEDTIDVFQQQTG
 GVY

>TALL

SSPVKRQRMESALDQLQFTTVVADTGDFHAIDEYKPQDATTNPSLILAAAQMPAYQELVEEAIAY
 GRKLGGSQEDQIKNAIDKLFVLFGAEILKKIPGRVSTEVDARLSFDKDAMVÄRARLIELYKEAGI
 SKDRILIKLSSTWEGIQÄKELEEQHGIHCNMTLLFSFAQAVACAEAGVTLISPFFVGRILDWHVAN
 TDKKSYEPLLEDPGVKSVTICKIINYKKFSYKTIVMGASFRNTGEIKALÄGCDFTISPKLGEELLQD
 NAKLVPVLSAKAAQASDLEKIHLDÉKSFRWLHNEDQMAVEKLSDGIRKFAADAVKLERMLTERMFN
 AENKG

>TCPG

QTDIRITREEDFTRILQMEEEYIQQLCEDI IQLKPDVVITEKGISDLAQHylMIRANITAIRRVRKT
 DNNRRIARACGARIVSRPEBLREDDVGTGAÄLLEIKKIGDEYFTFITDCKDPKACTILLRGASKEIL
 SEVERNLDQAMQVCRNVLLDPOLVPGGÄSEMAVAHALTEKSAMTGVEQWPYRAVAQÄLEVIPRT
 LIQNCASTIRLLTSIRAKHTÖENCETWGVNGETGTLVDMKEI.GIWEPLAVKLQTYKTAVETÄVLL
 LRIDDIVSGHKKKGDDQSROGGAPDAGQE

>VIM

SPQRSSRAPTTTHRALVRLFSGSQSAPPSSPRPSPPSAAMSTRSVSSSSYRRMFGGPGTÄSRPS
 SSRSYVTTSTRYSLGSALRPSTSRSLYASSPGGVYATRSSÄVRLRSSVPGVRLLQDSVDFSLADA
 INTEFKNTRTNEKVELQELNDRFÄNYIDKVRFLÉQONKILLAELEÖLKQÖGKSRLGDLYEEEMREL
 RRQVDQLTNDKARVEVERDNLAEDIMRLREKLOREEMLOREEAENTLOSFRQDVDNAÄSLARLÄDLERK
 VESLQEEIAFLKKLHEEEIQELQAOQJOEÖHVQIDVDVSKPDLTAALRDVRQOYESVAAKNLQHAE
 WYKSKFADLSEAANRNNDALROAKQESTEYRRQVQSLTCEVDALKGTNESLERQMREMEENFAVEA
 ANYQDTIGRLQDEIÖNMKEEMARHLREYQDLLNVKMA LDIEIATYRKILLEGEESRISLPLPNFSSL
 NLRETNLDLSPILVDTHSKRTLLIKTVETRDGQVNETSQHDDLE

>VIMC

QEEMILOREEAENTLOSFRQDVNAÄSLARLÄDLERKVESLQEEIAFLKKLHEEEIQELQAOQJOEÖHVQ
 IDVDVSKPDLTAALRDVRQOYESVAAKNLQHAEEWYKSKFADLSEAANRNNDALROAKQESTEYRR
 QVOSLTCEVDALKGTNESLERQMREMEENFAVEAANYQDTIGRLQDEIÖNMKEEMARHLREYQDLL
 NVKMA LDIEIATYRKILLEGEESRISLPLPNFSSLNLRETNLDLSPILVDTHSKRTLLIKTVETRDGQ
 VINETSQHDDLE

Figure 6 (continued)

>ZHX1

EQTINDLTDFGSFVKEENAEQAESTEVSSSGISISKTPIMKMMKNKVENKRIAVHHNSVEDVPEEK
ENEIKPDREEIVENPSSSASESNTSTSIVNRIHPSTASTVVTPTAAVLPGLAQVITAVSAQQNSNLIP
PKVLIPVNSIPTYNAALDNNPLLNTYNKFPTPYPTMSEITVLSAQAKYTEEQIKIWFSAQRLKHGV
WTPEEEVEEARRKQFNGTVHTVPQTITVIPTHISTGSNGLPSILQTCQIVGQPGVLTVAGTNTLP
VTAPIALTVAGVPSQNNILOKSOVPAOPTAETKPATTAAPTSQSVPKHEITALVNPDSEFGIRAKKTKE
QIAELKVSYLNQFPHDSEIIRLMKITGLTKGEIKKWFSDTRYNQRNSKSNOCLHLNNNDSTTIII
DSSDETTESPVTGTAQPKQSWNPFDFTPKFKEKTAEQLRVLQASFLNSSVLTDDEELNRLRAQTK
LTREIDAWFTEKKKSALKEEKMEIDESNAGSSKEEAGETSPADESGAPKGSGSTGKICKKTPEQI
HMLKSAFVRTQWPSPEEYDKLAKESGLARTDIVSWFGDTRYAWKNGNLKWYYYYQSANSSSMNGLS
SLRKGRGRPKGRGRPRGRPRGSKRINNWDRGSPSLIKFKTGTAILKDYYLKHKFLNEQDILDELV
NKSHMGYEQVREWFAERQRSELGIELFEENEEDEVIDDQEEDEEETDDSDTWEPPRHVKRKLSK
SDD

>ZNF33B

CYECGKTFCLKSDLTIHQRTHTGEKPFACPECGKFFSHKSTLSQHYRTHTGEKPYECHECGKIFYN
KSYLTKHNRHTGEKPYECNECGKTFQKSQQLTQHQRIHIGEKPYECNECGKAFCHKSALIVHQRT
HTQEKPYKCNECGKSFCKVKGGLILHERKHTGEKPYECNECGKSFSHKSSLTVHYRAHTGEKSCQCN
ECGKIFYRKSDLAKHQRSHTGEKPYECNTCRKTFQKSNLIVHQRTIGEKPYE

Figure 6 (continued)

>ALEX2

GGCGAATCAGTAGTTGGGGCTGCAATGGCTTCTGCAATAGCACCACCTCCGGGTGACAGAGGCC
 CTTGGGGCTGCAAGACCCCTGCAATGGCAGGGCTCCAAAGTGGCAGAAGCTCCAGAGAGAAGCG
 GAGACTTCCAGGGCAGCGGTGCGCTCCTGGGACAGTGGTGCCTACCGAAGCGGCAGCACCACTGAG
 GTGACCGAGGGTCTGGGTAGCAGCACCTACCAAGGTAGCTGAAGCTCCGGGTGGCATCGCCT
 ACCGAGGCAGCTGAGGCTCCTGTGCCCAGCAACGCCTACTGGGGCTGAGCACCTACTGGGGCTGCA
 GAGCTCTGGAACTCTGGTCCCTAGAACAGGGTGTTCTGGAACATCAGCTGCCAAGAAA
 GCAACCCCTGGGCTCACACTGGGCTATAACGAAAGCCACATCAGGAGCTGGAGCGGTACCCAAA
 GGTGGAGGCAGGGTGAACCAAGGTCCCGGAATGGGGCAAGGGCAAGGGAAAGAAAAGCAAAAGTT
 GAAGTAGACGAACTGGGGATGGGCTTCCGTCTGGAGATGGGGCTGCAGCAGCTGCTGCAGCCTCT
 GCTAAATGGCGGACAGGCTTCCCTGGCAGAGGTCCCTGATTCTGAGGAAGGGAGTCCGGTGGACT
 GACACAGAGTCAGATTCAAGACTCTGAGCCCCAGACCCAGCGCAGAGGGAGGGAAAGAACCCGTT
 GCGATGCAGAAGCGCCCTTCCTTATGAAATTGATGAGATTCTGGGTGTCCCGATCTCAGGAAG
 GTCTTGCCCTGCTTCAGAAATCTGATGATCCTTCATCCAACAGGTAGCTTGCTCACTCTGAGC
 AACAAATGCCAATTATTCAATGCAATCAAGAGACAACTCCGAAATTGGGAGGCCCTCCAATTATTGCA
 AACATGATCAACAAAATGATCACACATTAAGGAAAAGCCTTAATGCCATGAATAACCTGAGT
 GAGAATTATGAAAATCAGGGCCGGCTCAGGTGTACATGAATAAAAGTGTGATGGATGATATCATGGCC
 TCTAACCTGAACTCAGCAGTTCAAGTAGTTGGACTAAAATTCTAACAAACATGACTATTACTAAT
 GACTACCAACACCTGCTTGTCAATTCCAATGCAAACTTTCCGTTGCTATCTCAGGGAGGTGGA
 AAAATCAAGGTTGAGATTGAAAATCCTTCGAATTGCTGAAAATCCAGATATGTTGAAGAAA
 CTTCTCAGTACCCAAAGTGCAGCATCTTAGTTCCCTCTATAATTCTTACGTGGAATCAGAAATC
 CTTATTAAATGCCCTACTCTATTGAGATTATCTATGACAATCTCAGAGCAGAAGTGTAACTAT
 AGAGAATTCAATAAAGGTTCCCTTTTACTTATGCACTACATCTGGAGTGTGTTAAGAAAATT
 AGAGCCTTAGCAAATCACCATGACCTCTAGTGAAAGTTATAAAACTAGTGAACAAATTC

>APP1

GAGGAAGAGGGAGGAATCCTTCCACAGCCAGTAGATGATTACTTCGTGGAGCCCTCCGAGGGCTGAA
 GAGGAAGAGGAAACGGTCCCACCCCCAAGCTCCCATACACTTGCAGTGGTCGGAAAGTCACCTCC
 ACCCCGAGGCCACAGACGGTGTGGATAATTACTTTGGCATGCCCTGGGAAATCAGTGAGCACGAG
 GGGTTCCCTGAGGGCCAAGATGGACCTGGAGGGAGCGTAGGATGCGCCAGATTATGAGGTGATGCGT
 GAATGGGCCATGGCAGACAACCAGTCCAAGAACCTGCCATAAGCCGACAGACAGGCCCTGAATGAG
 CACTTCCAGTCCATTCTGCAAGACTCTGGAGGGAGCAGGTGTCTGGTGAAGCGACAGCGCCTGGTGGAA
 ACCCACGCCACCCCGCGTCATGCCCTTATCAACGACCAGGCCGGGCTGCCCTGGAGGGCTTCCCTG
 GCAGCCCTGCAGGCAGATCCGCTCAGGGAGGGCTGTCTGGCCCTGCGCGCTACCTGCGT
 GCGGAGCAGAAGGAACAGAGGCACACGCTGCCACTACCAGCATGTGGCCCGTGGATCCCGAG
 AAGGCACAGCAGATGCCCTCCAGGTGCATACCCACCTCAAGTGATTGAGGAGAGGGTGAATCAG
 AGCTGGGCCTGCTTGACCAAGAACCCCCACCTGGCTCAGGAGCTGCAGGCCCAATCAGGAACCTC
 CTCCACTCTGAACACCTGGGTCCAGTGAAATTGGAAGGCCCTGCCCTGGGGCAGCAGCGAGGAC
 AAGGGTGGCTGCAGCCTCCAGATTCCAAGGTGACACCCCCATGACCCCTCCAAAAGGGTCCACA
 GAACAAGATGCTGCATCCCCTGAGAAAGAGAAGATGAAACCCGCTGGAACAGTATGAGCGAAAGGTG
 AATGCGTCTGTTCCAGGGTTTCCCTTCCACTCATCGGAGATTCAAGAGGGATGAGCTGGCACCAAG
 CTGGGACAGGGGTGTCCTGAGGCTGTTGTCGGGTCTGC

Figure 6 (continued)

>BAI P1

CGGCCGCGGACGAAGATGGCACGCCATGTACTGGAGCACTATCTGGACAGTATCGAGAACCTT
 CCCTCGAACTTCAGAGGAACCTCCAGCTGATGCGAGAGCTGGACCAGAGGACGGAAGATAAGAAA
 GCAGAGATTGACATCCTGGCTGCAGAGTACATCTCCACGGTGAAGACGCTGTCTCCAGACCAGCGC
 GTGGAGCGCTGAGAAGATCCAGAACGCTACAGCAAGGAATACAGTGACGACAAAGTG
 CAGCTGGCCATGCAGACCTACGAGATGGGATAAACACATCGAAGGCTTGATGCAGACCTGGCG
 CGCTTGAAGCAGATCTGAAGGACAAGATGGAGGGCAGCATTGAAAGCTCCGGAGGGCAGGG
 TTAAGGAGGCGGGTCAGAAAGAAAAAGAGGGTCCCAGGGCAGGAGGACATCAGAG
 GAAGACACACCAAGAAAAAGAACAAAGGAGGGTCTGAGTTCACTGACACCACTCTGCTCCGTG
 CACCCCTCTGATGTGCTGGACATGCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAG
 GTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTCACTTGCC
 TGCGTGGACCTTACACGAAACCAAAGGAAAATGG

>BAI P2

AGCCAGCAGGCCAGCGTACCATGCAAGATGTGGAGCGCGAGTCCTTCGAGGTGTTGGTCGACTAC
 TGCTACACGGGTCGTGTGTCCTCAGTGAGGCCAATGTGCAGCGCCTGTACGCCCTCCGACATG
 CTACAGCTGGAATATGTGCGGGAGCCTGCGCTCCCTCTTAGCCCGACGTCTGACCTGACCAAC
 TGCAACGCCATCCTCAAGTTGAGACGCCCTGACCATCACAAGCTCGATCTCAGGCCAGTCC
 TACATAGCTCACAACTTCAAGCAGCTCAGCGAATGGGTTCAATTGGGAGGAGACTCTAGCAGAT
 CTAACCTGGCCAGCTGCTGGCTGTCTACGCCCTGGATAGTCTGGACATAGAGAGTGAGCGGACT
 GTATGCCATGTAGCTGTGCACTGGCTGGAGGCTGCTGCCAAGAGCGGGTCCAGTGCTGCAGAA
 GTCTTCAAGTGCCTGCGCTGGATGCACTCACTGAAGAAGATCAGGACTACTTAAAGGGCTGCTG
 ACCAAGCCCACGTGAAGAAGTACTGCCTGGACGTTATTGAAGGGGCCCTGCAGATGCCCTATGGT
 GACCTGTTGACAAGTCTCTGGGCCAGGCCAAACAGCAGCAGCAGTAGCAGCAGCAACTCT
 CTTGTATCTGCAAGCAGAAAATCCACCCAGAGACTGGGTATGTGTCGCAAGGAGATGGTATCTTC
 TTTGGACATCCTAGAGATCCCTTCTGCTATGACCTTACTCGGGGACATTACACAAATGCCA
 TCCCCTTGACCAGCTTGCTCACACTAAGACTGTCACCTCTCAGCTGCTGTGTCCTCCAGAC
 CATGACATCTATCTAGCTGCTCAGCCCAGGAAAGACCTCTGGGTGTATAAACCAAGCTCAGAATAGT
 TGGCAGCAACTTGCAGATCGCTTGCTGTGAGGGCATGGATGTGGCATATCTCAATGGCTAC
 ATCTACATTGGGGGACGAGACCTTACTGAGTTAAGTGAAGGAAGTGGAAATGCTACAGT
 GTTCAGAGAAACCACTGGGATTGGTGGCTCTGCTCCCTCAATTCTCTATTCTTTGAACCTCATA
 GTGGTTCAAGAACTATCTTATGCTGTCAACAGTAAGCGCATGCTTGCTATGACCTAGCCACAAT
 ATGTGGCTGAACCTGTGCTTCTCTAAACGTAGTGACTTTGAGGACATGTGCTTCAATGATGAA
 ATCTATTGTATCTGTCGACATCCAGTCAGGATCTACAACCCAGCTAGGGGAGAATGAGGGCG
 ATTAGTAATATTCTTGGATTCAAGAGACCCACAACCTACAGATTGCAATCATGACCAAAGTTG
 CTTCTCATCACTTCTACAACCCACAATGGAAAAGAACCGAGTGACAGTGTATGAGTATGATACT
 AGGGAAAGATCAGTGGATTAAATATAGGTACCATGTTAGGCCTTTGAGGTTACTCTGGCTTATT
 TGCCTTGTGCTCGTGTATTACCTCTGCAACCTGGTCAGAGTTTATTACTGAGGAAGAT
 GATGCCACGGAGTGAGTCTAGTACTGAATGGACTTAGATGGATTCACTGAGCTGGACTCTGAGTC
 GGAAGTTCAAGTTCTTTTCAGATGAGTCAAGTCTGGGTGCAAGTAGCACCTCAGCGAAATGCAACAG
 GATCAGCAGGGTTCTTG

Figure 6 (continued)

>BAIP3

GGACACAATGCCCTCAGAAAAGTAACAGCCGTCACTTATGCTAGAAAAGGAAGTGTCCCTCAGAGC
 ATAGAGAAAATAAGTTCTCTGTTGATGCAACAACGTGTTACTTCACAAACAGTGTGTTTCAGAGAC
 CAAGAACCAAGATCCATAATGAGATGGCATCAACATCAGATAAAGGTGCCAAGGAAGAAATGAC
 AAGAAAGATTCTCAAGGAAGAAGTAATAAAGCATTACATCTGAAGAGTGTGATGCTGAATTAAAAG
 ATATTGGCCTTACTAAGGATTGAGAGTGTGCTTACTCGAATTCCGTACCATTTGACCTCTGGA
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 AGTCACAGCAGAAAACCAGACAGAAGAAAAGAGAACTGAGATGGAATACTATACCCATGAGAAGCAAGAG
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>BARD1

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 GGAAAACGTGCCATCACAATAGACTTCCAGTCCCATTCTAAGAGATGTAGAACCCAGCATTCTG
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>CA150

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 AAGAAAAGTGGACCCAACTCCGACAATGCTGTCGATCCAAAAGTGGCAATTCTCTATGAGTGCA
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 AAG

Figure 6 (continued)

>CGI-125

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>CGI-74

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 AAAAGG

>CLH-17

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 CTTGAGACT

>CLK1

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 CAGAAAACCAAGGAAACGTAATATTTCAACCACGATCGATTAGACTGGGATGAAACACAGTTCTGCC
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Figure 6 (continued)

>DRP-1
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CGCTCCAACATCACCAAGCCTCGGT
>EF1A
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>EF1G (bait)
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GTCTTCCGAGGCCAGGAGCTGCTCTTCCGCTGAGTCCAGATTGGCAGGTGGACTACGAGTCATAC
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Figure 6 (continued)

>EF1G (prey)

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>FEZ1

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>G45IP1

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Figure 6 (continued)

>G45IP2

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>G45IP3

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 AACACGGAGAAAGCACATACCAAGGCCAACACACACCACCTGTCCAAAAGGCCCTCGATAACGGGAT
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 CCTAGCCCTACCCCCCAATTAGGAGGGCACTGGCCCCAACAGGCATACCCCGCTAAATCCCCT
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>GADD4.5G

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Figure 6 (continued)

>GIT1

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 GGGCGACAAAAGCTGGCCCGCTTTAATGCCCGAGAGTTGCAACCTTGATCATGACATTCTCAGT
 GAGGCCAAGCCGAGACAGCAGGCCAGAGACAACCTCGAGCTGCTCTG
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 >hADA3

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 GAGCTCGCAAACGGCAGGCTGAGCTGAAGGCACCTAGTGCCTCACAAACGCCACCAAGAACGAC
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 AACGAGGTGATGGACGCCCTTCGCAAGATCATGGCTGCCCGGAGAACAGCGGACTCCCACCAAG
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Figure 6 (continued)

>HBO1

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 GGAAAACACCTAGTTAAAGAGACAGGACCTGATTGATGAGTGGATAGGCCAAAGAGGCCAAAGG
 TCCAACCTCAATAAACCATGGATCCCCAGCTGCTTAAATGGACCCCTCCCAAGGGCACT

Figure 6 (continued)

>HD1.7

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 CAG
 CCGCCGCCGCCGCCCTCCTCAGCTTCCTCAGCCGCCGCCAGGCACAGCCGCTGCTGCCCTCAG
 CGCAGCCGCCGCCGCCGCCGCCACCCGGCCGGCTGAGGAGCCGCTGAC
 CGACCAAAGAAAGAACTTCAGCTACCAAGAAAGACCGTGTGAATCATTGCTGACAATATGTGAA
 AACATAGTGGCACAGTGTGTCAGAAATTCTCCAGAAATTCTAGAAACTCTGGGCATCGCTATGGAA
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 GTTGGCCCTCAGAAATGCAAGGCCCTACCTGGTGAACCTTCTGCCGTGACTCGAACAAAGCAAG
 AGACCCGAAGAATCAGTCCAGGAGACCTGGCTGCAGCTGTTCCAAATTATGGCTTCTTGGC
 AATTGGCAAATGACAATGAAATTAAAGGTTTGTAAAGGCCCTCATAGCGAACCTGAAAGTCAAGG
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 GCAGAGCAGCTTGTCCAGGTTATGAACTGACGTTACATCATACAGCACCAAGACCACAAATGTT
 GTGACCGGGAGCCCTGGAGCTGTTGCAAGCAGCTTCAAGAACGCCCTACCCGGAGCTCTGCAAACC
 CTGACCGCAGTCGGGGGCAATTGGCAGCTACCGCTGCTAAGGAGGAGCTGGTGGCCGAAGCCGT
 AGTGGGAGTATTGTGGAACTTATAGCTGGAGGGGGTCTCATGAGCCCTGTGAGGATGACTCTGAATCGAGATCGGAT
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 GTCAGCAGCTGCCTAACAGCTCAGTGAAGGATGAGATCAGTGGAGAGCTGGCTGCTCTTCA
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 GCAGGGGACTCAGTGGATCTGGCAGCTG

>HDD1.0

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 CGCAGCCGCCGCCGCCGCCACCCGGCCCTGTGGCTGAGGAGCCGCTG
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 AATTGGCAAATGACAATGAAATTAAAGGTTTGTAAAGGCCCTCATAGCGAACCTGAAAGTCAAGC
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Figure 6 (continued)

>HDd1.3

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TTAAGGCCCTCATAGCGAACCTGAAGTCAGGCTGGGACAGGGCTGATCA
 GCAGTGAGCATCTGCCAGCACTCAAGAAGGACACAATTATTCATAGTGGCTACTAAATGTGCTC
 TTAGGCTTACTCGTTCCGTGAGGATGAACACTCCACTCTGCTGATTCTGGCGTGCTGCTCACC
 CTGAGGTATTGGTGCCCTGCTGAGCAGCAGGTCAAGGACACAAGCCTGAAAGGCAGCTCGGA
 GTGACAAGGAAAGAAATGGAAGTCTCTCCTCTGAGCAGCAGCTTGTCCAGGTTATGAACGTGAGC
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 TTCAGAACGCCCTCACCCGAGCTTCTGCAAACCCCTGACCGCAGTCGGGGCATTGGCAGCTCACC
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 GGTTCCCTCATGCAAGCCCTGCTTCAAGAAAACAAAAGGCAAAGTCTCTAGGGAGAAGAAGAA
 GCCTTGGAGGATGACTCTGAATCGAGATCGGATGTCAGCAGCTCTGCTTAACAGCCTCAGTGAAG
 GATGAGATCAGTGGAGAGCTGGCTGCTTCTCAGGGTTTCACTCCAGGGTCAAGCAGGTCAATGAC
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>HDexQ20

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>HDexQ51

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>HIP1

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 GCCCAGTCAGAACAGCTGGCCAGGAGTTGCGCAGCTAGAGAAGGAGCAGGGACAGCCTGGTG
 AGTGGCGAGCTCATAGGGAGGAGGAATTATCTGCTCTCAGGAAAGAAACTGCAGGACACTCAGCTC
 AAACAGGCCAGCACAGAGGAATCTATGTGCCAGCTGCCAAAGACCAACGAAAAATGCTCTGGTG
 GGGTCAGGAAGGCTGCCAGGAGCTGCGGAGCAGGTGATAACAAGACGCCGTCACGCCCG

Figure 6 (continued)

>HIP11

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 AGCCTGGTCAACGAGCTGGCCTCACCGCCCGCAAGATGATGGCTGACGAGGCCCTGGCAGTGGG
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>HIP13

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 AGCCCTGAGTCGCCATCTGTTGAGGGCCCCAAGGTGTCACCAGCATGCCCTCCTCAATGTGG
 AGCGGCCAAGCTTCCGTTAACCCCTCCACTTCCAGGCCGAAGCCAGTATCCCTGAGGAGCACAGA
 CAGGCAATTCCAGAAAGTGAAGCTGAAGACCAGGAACGGGAAACCCCCAAGTGCCTACTGTCCTCCCA
 GGCAGATTCCAGAGAGTGAACCTGAGACCTGAGGCCAAGGGATACTCCACAAGGAGAACATG
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 TTTCT

>HIP15

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 ACTATGACTATTGACTATCACACACTGATTGCCAACTATATGTCGGGTTCTCTCCTTATTAACC
 ACAGCCAATGCGAGAAGCAAGTTCACGTTCTGAAAATGCTATTGAAATTGTCGAAAATCCTGCT
 GTGGCAAAAAAACTATTCACTGCAAAGCTCTTCAATATTGTCGGGCTCTTAAACATAGAAGAG
 ACAAAATGATAATATTCAAATTGTTATTAAAATGTTCAGAATATCAGTAACATTATAAAAGTGGG
 AAGATGTCCTTAATTGATGATGATTTCAGTCTTGAGCCGTTATTCTGCATTGTCGAAATTGAG
 GAGTTAGCTAAGCAACTACAAGCCAAATAGACACCAAAATGATCCTGAGGTGGACAACAAAGT

>HIP16

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 CCTGGCTGGGGCAGTGGGTGGCTCAAAGCCAGTGCCTAAAGGCCAAGAAAAGACGCCGTTCTC
 ATTAAGCCCTGAGGGTCTCCAAGAAAAGATAAGAATTGCCAAATGTGATTATCAATGAGAAG
 CGCAACATCCACGCCAGCTGCTCATCAGGTACGAGTGCCTCCATATCCATTACCCACCATTGGCAA
 TTTGAAAGGACCATCCAGACCCCCATAGGATCCACATGGAACACCCAGAGGGCTTCCAAAAGCTG
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>HIP2

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 AGTAACGT

Figure 6 (continued)

>HIP5 (bait)

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 GAAAAGGTGCAGAAATTCAAAGACTATTAAAAACTGAGGTGGTTGATGAAACTAGCAATATA
 GAAAACAATGCTGAAAACAGTCATTCACTGAAGAATAAAACAGGAACAACACTCAACAGCATTCTCAA
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 GCTGATACAAAGAAGTCCAGGGAGGATTCTATCTGAAAATGTTACGACTTTAGGAGGATCTGGA
 GCAGACCATATGCCTTGAACGTGTTTATACCTCAGGTATATAACTTGCTAAACATGCCTGGCCA
 GCCTCAAAAAAGAAGAAAGTAAAATCCCTGTACATGATGATTCTAAACTAAGCAAGGTAAAGCCA
 CAAAGAGGTAGAGCAAAATAATTAGAAAACCAGGATCTGAAAAGTCAAATCAGGCTTATATGT
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 CAGGGAAAATTAAATTATACCTTGTCTCCTCAATCTACATCAAATATTAGAAGTGGTAAAAAT
 ATACAAGTGTCTAGTGTCAAGGAGTAACCTCTGAAAATCCTCAAACATATTACACATAACTCT
 TTTAATTCAAACATGTGCTTCAACAGAACACAGTTGAAATCAGTGGAAATCAGGAAAGTAGTTCT
 CCACTCTCAAATGCTTGTCTGACCTAGTCACGTGATACCATCACTGCCATCATATTGTTCTCA
 GAGTGCCTAAACTTGCCTAAATCATTCAAATGGCACTCAAGCAGTTGCCCCGGCAAGATGCG
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 GATAGTACTTCTGAGTTTTGATGGCTGAAAATTAGTGAAGCATTAGTGCCTGAGGATGAGATT
 CTGACTGTCTGAAATACCAAACAGATAAGAAATCAAATCTACCTTAAATAAAACTCAACAAATT
 AACATCTGCACACTGTGCAAGAACAGATCCTAGAGTCCCTTAATGATCTCAATGAAAGA
 CTACATTATATAAGAATCCATTGCAAAACCCATCCATCAAATAACTTTACAAATAATACCA
 CTTCTGGAGAAGAGAGAAGATAGAACCGAGCAGCTGAGAGACAAGAGA

>HIP5 (prey)

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 GAAAAGGTGCAGAAATTCAAAGACTATTAAAAACTGAGGTGGTTGATGAAACTAGCAATATA
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Figure 6 (continued)

>HMP

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CCTCATATAACTGCTGCAGAGGGTAAACCTCACACATGATAGTTGATCTGGATAATGTGGTCAAA
AAGGTCCAAGCAGCTCAGTCTGAGGCTAAGGTTGATCTCAGTATCATGAGCTGGTGGTCCAAGCT
CGGGATGACTTTAACGAGAGCTGGACAGTATTACTCCAGAACATGCTCTCTCTGGTGGAAAGGAATG
AGTGTTCAGACTTAGCTGACAAGCTCTACTGATGATCTGAACACTCCCTCATGCTCATGCACAT
CGTCGTATTGATCAGCTAACAGAGAGCTGGCAGAACAGAACAGGACACCGAAAAGCAGCACATCACG
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>HP28

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Figure 6 (continued)

>HSPC232

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GTGGTGAAATGCTGATTGAAAAGATCCTCATAGAAAAGCTATACAGTTGATTGAGGAG
AATTACATGAAATAGGTGAGCGGTGTTGAAAGAACTCAAGCATTGAGAGTATGATACT
TCCACTCAAGATTGGAGAGCCTTT

>HYPA

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>HZFH

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 GTAGGGGCCCTGGCCGCCAGGCCAATTACAGCCAGATGCTGCAAGGTTCTCATCACAGCC
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Figure 6 (continued)

>IKAP

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 AGTATCATGGCATCTTATCAGCAACAGAAGACTTCGGTTCCCTGTTCTGATGCTGAGCTTTTATA
 CCACCAAAGATCAACAGAAGAACCCAGTGGAGCTGAGCCTGCTAGAC

>IMPD2

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 ATGGCCATAGCAATGGCCTTACAGGCGTATTGGCTTCATCCACCACAAGTACACCTGAATT
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 AGCCCCAAGGATCGGGTGGGGATGTTTGAGGCCAAGGCCCCGGATGGTTCTGCGGTATCCCA
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 GACTACCCACTAGCCTCCAAAGATGCCAAGAACAGCTGCTGTGGGGCAGGCATTGGCACTCAT
 GAGGATGACAAGTATAAGGCTGGACTTGCTGCCAGGCTGGTGTGGATGATGAGTGGTTTGACTCT
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 GCCCTGCCGGTGGGCATGGGAAGTGGCTCCATCTGCATTACGCAGGAAGTGCCTGGCTGTGGCG
 CCCCAAGCAACAGCAGTACAAGGTGTCAGAGTATGCACGGCGCTTGGTGTCCGGTATTGCT
 GATGGAGGAATCCAAATGTGGGTCAATTGCGAAAGCCTGGCCCTGGGGCTCCACAGTCATG
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 TCAATCCACAAATTGTCCCTTACCTGATTGCTGGCATCCAAACACTCATGCCAGGACATTGGTGC
 AAGAGCTTGACCCAAAGTCCGAGCCATGATGIACTCTGGGAGCTTAAGTTGAGAAGAACGTCC
 TCAGCCCAGGTGGAGGTGGCTCATAGCCTCATTGATGAGAAGCGGCTTTTC

>KPNA2

GCTTGGGCACTCACTAACATTGCTTCTGGGACATCAGAACAAACCAAGGCTGTGGTAGATGGAGGT
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 GCTCTAGGAAACATTGCAAGGTGATGGCTCAGTGTCCGAGACTTGGTTATTAAAGTACGGTGCAGTT
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 GTGCCCAACTTGTGAAGCTTCTAGGAGCTCTGAATTGCAATTGTGACTCTGCCCTAACAGGCC
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 GAGAACAGTCAAACGTTGTACAGAAAACCTGAGTCTGTGTATAAGGCTTGTAAAGCTTAATT
 GAGAAGTATTCTCTGTAGAGGAAGAGGAAGATCAAACGTTGTACAGAAAACACCTCTGAAGGC
 TACACTTCCAAGTTCAAGGATGGGCTCTGGACCTTTAACTTT

Figure 6 (continued)

>KPNB1

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 GTTGTATTGAACTCTTCAGCAGGCCCTCCAAGGCCAGGTGGACAAGTCAGACTATGACATGGTG
 GATTATCTGAATGAGCTAAGGAAAGCTGCTTGGAAAGCCTAACTCGAATCGTCCAGGGATTAAAG
 GGGATCAGGAGAACGTAACCCGGATGTGATGCTGGTACAACCCAGAGTAGAAATTATTCTGTCT
 TTCAATTGACACATTGCTGGAGATGAGGATCACACAGATGGAGTAGTAGCTTGTGCTGGACTA
 ATAGGGGACTTATGTACAGCTTGGGAAGGATGTACTGAAATTAGTAGAAGCTAGGCCATGATC
 CATGAATTGTTAACTGAAGGGCGGAGATCGAAGACTAACAAAGCAAAACCCCTGCTACATGGCA
 ACAAAAGAAGTGGAGAACTGAAGAACCAAGCT

>KU70

AAGACCCGGACCTTAATACAAGTACAGGCCGTTGCTTCTGCCAGCGATACCAAGAGGTCTCAG
 ATCTATGGGAGTCGTCACTTAACTGGAGAAAGAGGAAACAGAACAGAGCTAAACGGTTGATGAT
 CCAGGTTTGATGCTCATGGGTTCAAGCCGTTGGTACTGCTGAAGAACACCAATTACCTGAGGCC
 TCCCTGTCGTGTACCCAGAGGAGTCGCTGGTATTGGAGCTCAACCTGTTAGTGCCTGCTC
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 TATTTGTGGCTTTGGTGCACAGGAAGAAGAGTTGGATGACCAGAAAATTCAAGGTGACTCCCTCA
 GGCTTCCAGCTGGTCTTTTACCTTGTGATGATAAAAGGAAGATGCCCTTACTGAAAAAAATC
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 GAGCTGAAGACCCACATCAGCAAGGGTACGCTGGCAAGTTCAGTGTGCCATGCTGAAGAGGCC
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 TTCAGGAC

>LUC7B1

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 CTTGGTCTCCATGACAATGACCGTGCCTGGCAGACCACTCGGTGCCAGTTACACTTGGGTT
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 CAGGATCGCTTGAGGAGAGAGGAGAGGGAACGGGAGGGCTTGAGCAGGAGGTGGGATCA
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 CGAGAGCGACGGAAATTGTCCCGGTCCGGTCCGAGATAAGACATCGGCGCCACCGCAGCCGTTCC
 CGGAGCCACAGCCGGGACATCGTCCGGTCCCGGACCGAAGTGCAGAAATACAAGTTCTCCAGA
 GAGCGGGCATCCAGAGAGGAGTCCCTGGAGAGCGGGCGGAGCGAGCGAGGGCCCCCGGACTGGAGG
 CTTGAGAGCTCCAACGGGAAGATGGCTTACGGAGGTAGAAAGAGAACAGGAGGCCGGAGATC

>MAGEH1

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Figure 6 (continued)

>MAP11c3

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 CCCACGCAGGCCCTCTCCTGCTGGTGAACCAGCACAGCATGGTGAGTGTCCACGCCA TCGCG
 GACATCTACGAGCAGGAGAAAGACGAGGACGGCTTCTCTATATGGTCTACGCCCTCCAGGAAACC
 TTCGGCTTC

>mHAP1

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 GAGGAGAATAATAAGCTGGAAACCATGCTGGCTCAGCCAGGGAGGAGATTTCACATCTCCGGAAG
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 GACGAGGAAGACGAGGAAGAGGGCGAAGAGGAGGACAGAGAAGGAGGATCAAGACACAGCAG
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 TCCACCTTGACAACCTGGAGGACGAAGAGCAGATGCTCATCTGGATGTGGAGCAGTTCTCT
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 GGGGCCAGACGGAGAAACTGCAGCAGATGCTGGCTCAGAGAAGGGATCCACTCGGAGAGCCTG
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 GCACCTCCAAGTTCCAGAGACACTGGCTGAGGAGCTCCGAACATCTCTGAGGAAGTTCACT
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 GCGATGCCACCCCCACCGGCTCA

>mp53

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 CCTGTCAGTTGTGGGTCAAGGCCACACCTCCAGCTGGAGCCGTGCGCCATGGCCATCTAC
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 GATGGCCTGGCTCCTCCCCAGCATCTTATCCGGTGGAGGAAATTGTATCCCGAGTATCTGGAA
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 CAAAAGAAAAACCACTTGATGGAGAGTATTCACCCCTCAAGATCCGGGGCGTAAACGCTTCGAG
 ATGTTCCGGGAGCTGAATGAGGCCCTAGAGTTAAAGGATGCCATGCTACAGAGGAGTCTGGAGAC
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 ATGGTCAAGAAAGTGGGGCTGACTCAGAC

Figure 6 (continued)

>NAG4

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AAAGAAAAGATCAAGAACAAATGACTATCAGTCCATAGAAAGAACTAAAGGATAACTTCAAACTAATG
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CCCTCATACAGAGAAATGCATCTGCTGAACAAAGTGACCAATAATCTAAAGAACTTGCACAGCAA
GTAAGTCCAGGTGATATCGTAAGCACGTATGGAGTTGAAAGCAATGGGATTCCATTCTTCC
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GCTGAGTGTGGACCTGGTGGAAAGT

Figure 6 (continued)

>NEFL

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 GAGCTGGAGCAGCAGAACAAAGGTCTGGAGGCCAGGACTCGCTGGTGTGCGCCAGAACGACTCCGAG
 CCATCCCCTCCGGCGCTGTACGAGCAGGAGATCCGCGACCTCGCCCTGGCGCGGAAGATGCC
 ACCAACGAGAACGAGCCAGGGCTCCAGGGCGAGCGCGAAGGGCTGGAGGAAGACCTCGCGAACCTGCAG
 GCGCGCTATGAAGAGGAGGTGCTGAGCCCGAGGGACGCCAGGGCCGGCTGATGGAAGCGCGCAA
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 CCGCTCTACTACACCAAGCCATGTCCAAGAGGAGCAGATCGAAGTGGAGGAAACCAATTGAGGCTGCC
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>p53

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 CCCAACACACCAGCTCTCTCCCCAGCCAAGAACAGAACACTGGATGGAGAACATTTCACCC
 CAGATCCGTGGCGTGAGCGCTCGAGATGTTCCGAGAGCTGAATGAGGCCCTGGAACTCAAGGAT
 GCCCAGGCTGGAGGAAGGAGCCAGGGGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAGG
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Figure 6 (continued)

>PFN2

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 AAAGACCGGGAAAGGTTCTTACCAACGGTTGACTCTGGCGCGAAGAAATGCTCAGTGATCAGA
 GATAGTCTATACTCGATGCTGACTGCCAAATGCCACATGGGACAAAGAGTCAGGTGGGAGCCA
 ACATACAATGTGGCTGCGCAGAGCTGCTAGAGCTTGGTCTTGTAATGGAAAAGAACGGGTC
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>PIASy (bait)

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 GCCGGCGCTGTGCCCAGGACTCCGCTGGCAGGCCCAATATTGACTACCCCGTGTCTACGGAAAG
 TACTTAAACGGACTGGGACGGTTGCCAGAACGCCCTCAAGCCAGAACGCTCCGCTGGTAAAGCTG
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 GTGCTGGGCCCTCGGACGCCAATGGGCTCTGCCGCCAGCGTCAACGGAGCGGTGCCCTG
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Figure 6 (continued)

>PIAsy (prey)
CTGGTGGAGGCCAAAAACATGGTGTGAGTTTCGAGTCTCCGACCTTCAGATGCTCTGGGTTTC
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TCGGAGCCTGCCACAGCCGACCCGGCCCTGGACCCCTGACCATGCACTCCACCTACGACCGG
eeeeeeeeGTGTGeeGAGGACTGGCTGGCACGCCCAATATTGACTACCCGTGCTACGGAAAG
TACTTAACGGACTGGACGGTTGCCGCCAAGACCCCTCAAGCAGAAGTCCGGCTGGTGAAGCTG
CCGTTCTTAATAATGCTGGATGAGCTGCTGAAGCCCACCGAATTAGTCCCACAGAACAAACGAGAAG
CTTCAGGAGAGGCCGTGCATCTTCGCAATTGACGCCAAGACAGGGAGTTGATCCGGAACCTCAGG
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>PLIP
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CTTGGCCTCTATCCTATCGAAGCTACTGGTCCCAGACCATCCTGGAGATCCTGATGGGCTGAAG
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GAGGATGTCACTCCACTGCACTGAGTACCTCAATCTCATCAACTACTACAAGGGCAAGTACATCCTC
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Figure 6 (continued)

>PTN
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CAACAGTACGGAGCAGCAGGGTCCAAAATTGCAAGCTGCCCTCTGGCATTCATTTCAACTGGCA
GCTGTGGATACTGCTGAAGCAGGGAAAGAAAGAGAAACCAGAAAAAAAGTGAAGAAGTCTGACTGT
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>PTPK
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>SETBD1
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CAATTCTATGATGGCAGGGAGTCTTGCTACATCATTGATGCCAAGCTTGAAGGCAACCTGGGCCG
TACCTCAACCACAGTGTGCAGCCCCAACCTGTTGTCAGAATGTCTTGTGGATAACCCATGATCTT
CGCTTCCCTGGTGGCCTTCTTGCCAGCAAAAGAATCCGGGCTGGACAGAACACTTACTTGGGAC
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Figure 6 (continued)

>SH3GL3

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>SUMO-2

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 CTGGCAGGGCACAGTTTC

>SUMO-3

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 GGTGTCTAC

>TAIL

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 AACGCCAACGCTGGTGGCTGTGCTCAGCCAAAGGGGGCCAAAGCCAGTGACCTGGAAAAATCCAC
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 GGGATCCGCAAGTTGGCGCTGATGCAGTGAAAGCTGGAGGGATGCTGACAGAACGAATGTTCAAT
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Figure 6 (continued)

>TCPG

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 CACAATAATCGCATTGCTAGAGCCTGTGGGGCCCGATAGTCAGCCGACCAGAGGAAGTGAAGAGAA
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 TCGGAAGTAGAACGCAACCTCAGGATGCCATGCAAGTGTGCAATGTTCTCCCTGGACCCCTCAG
 CTGGTCCCAGGGGGGGCTCCGAGATGGCTGTGGCCCATGCGCTGACAGAAAATCCAAGGCC
 ATGACTGGTGTGGAACAATGGCCATACAGGGCTGTGCCCAGGCCCTAGAGGTCAATTCTCGTACC
 CTGATCCAGAACTGTGGGGCCAGCACCATCCGCTACTTACCTCCCTCGGGCAAGCACACCCAG
 GAGAACTGTGAGACCTGGGTGAAATGGTGGAGACGGGTACTTGGTGGACATGAAGGAACGGC
 ATATGGGAGCCATTGGCTGTGAAGCTGCAGACTTATAAGACAGCAGTGGAGACGGCAGTTCTGCTA
 CTGCGAATTGATGACATCGTTCAAGGCCACAAAAGAAAGGCATGACCAGAGCCGGCAAGGC
 GCTCCTGATGCTGGCCAGGAG

>VIM

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 TCCGGGAGCCAGTCGGGCCACCGCCGCCAGGCCATGCCACCCCTCCGAGCCATGTCCACC
 AGGTCCGTCTCGTCTCCCTACCGCAGGAATGTTGGCGCCCGGGCACCAGCGAGCCGGCCGAGC
 TCCAGCCGAGCTACGTGACTACGTCCACCGCACCTACAGCCTGGCAGCGCGCTGCGCCCCAGC
 ACCAGCCGAGCCCTACGCCCTCGTCCCCGGGGGGCGTGTATGCCACCGCCTCTGCCGTGCGC
 CTGCGGAGCAGCGTGGCCGGGTGCGGCTCCTGAGGACTCGGTGGACTTCTCGCTGGCGACGCC
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 GAA

Figure 6 (continued)

>VIMc

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 CCTCTGGTTGATAACCACTCAAAAGGACACTTCTGATTAAGACGGTTGAAACTAGAGATGGACAG
 GTTATCAACGAAACTCTCAGCATCACCGATGACCTTGAA

>ZHX1

GAACAAAACAATAATGATCTGACTTTGATGGTAGTTTGTAAAGAGGGAGATGCAGAGCAAGCA
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 AATAAAAGTGGAAAATAAACGGATTGCAGTTCATCATAACTCAGTTGAGGACGTTCTGAAAGAGAAA
 GAGAATGAAATCAAACCAAGACCGTGAAGAAATTGTAGAAAATCCAAGTTCTCAGCTCTGAATCT
 AATACAAGTACTTCCATTGTAACAGAAATACATCCAAGTACTGCCAGCAGGTAGTGACACCAGCA
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 CCCAAAGTCTTAATCCCTGTTAATAGCATTCCCACCTACAATGCTGATTGGATAACAAATCCCCTT
 TTACTTAACACCTACAACAAGTCCCTACCCAAACAATGTCAGAAATTACAGTTCTCTGCTCAA
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 ACATGCCAATAGTTGGTCAGCCTGGCTGGCTTACTCAAGTGGCTGGAACAAACACCTTGCA
 GTTACAGCACCTATAAGCCTTGACAGTGGCAGGCCTTCAAAGTCAAAATAATATACAGAAAAGTCAG
 GTACCTGCTGCTCAGCCTACTGCAGAAACAAAGCCAGCAACAGCAGCAGTTCCAACCTCTCAAAGT
 GTCAAACATGAAACTGCATTGGTAAACCCCTGATTCAATTGGCATTGGGCAAAAGACAAAAGAG
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 TCAAGATGAC

Figure 6 (continued).

>ZNF33B

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GAATGTGGAAAATCTTTACCGTAAATCAGACCTTGTCTAACATCAGAGATCACATAACAGGGAA
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Figure 6 (continued)

Nucleotide sequence data (fasta format)

>GDF9

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>GAPD

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>MOV34

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CCGGTGCTCAGCACAGACAAGTCAAGACAGATTATGATCAATGCAACGACGTGGGCTCATGCCCTACCTC
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Protein sequence data (fasta format)

>GDF9

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>GAPD

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>MOV34

Figure 6 (continued)

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Figure 6 (continued)

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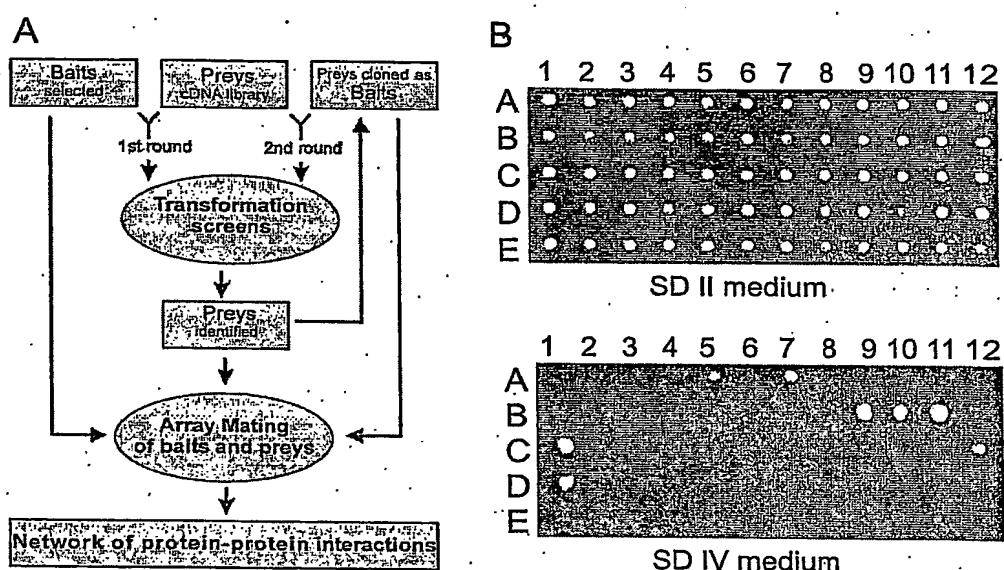
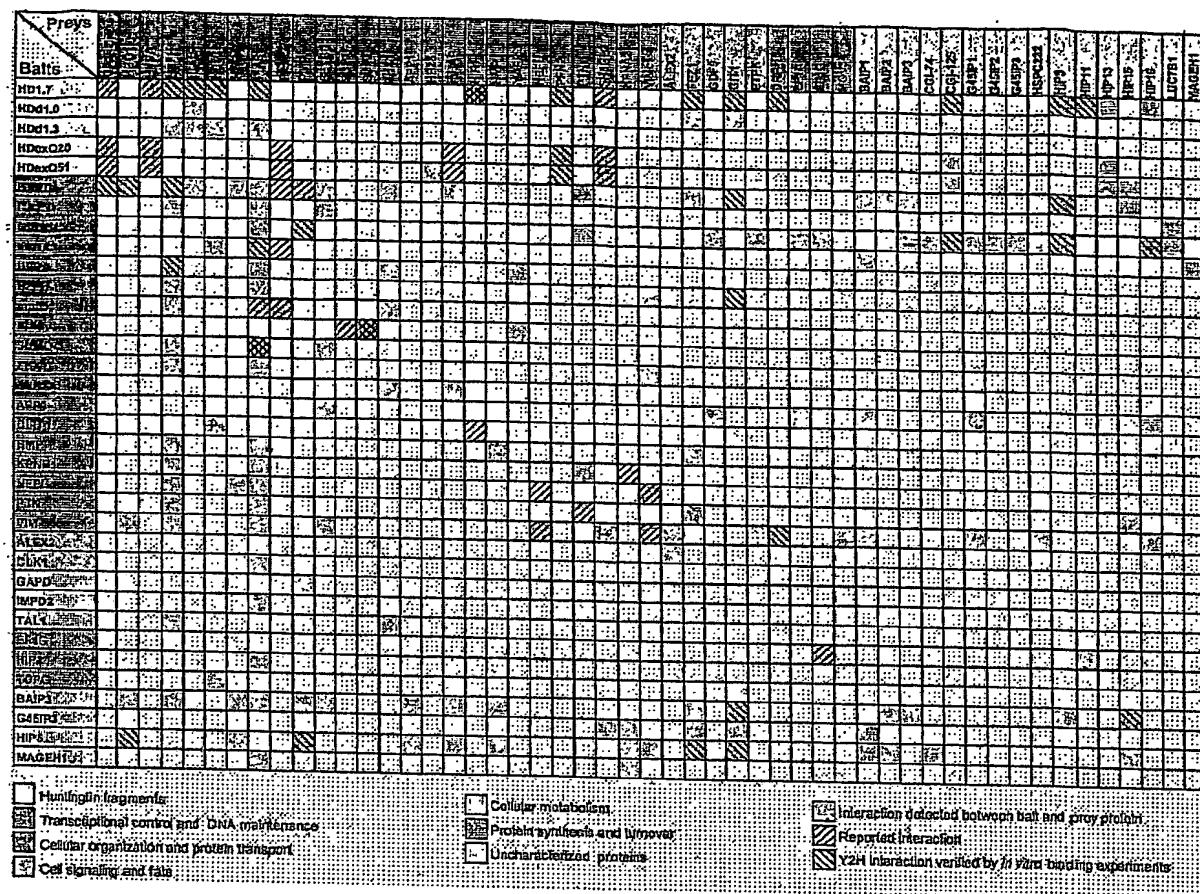


Figure 7

A



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B

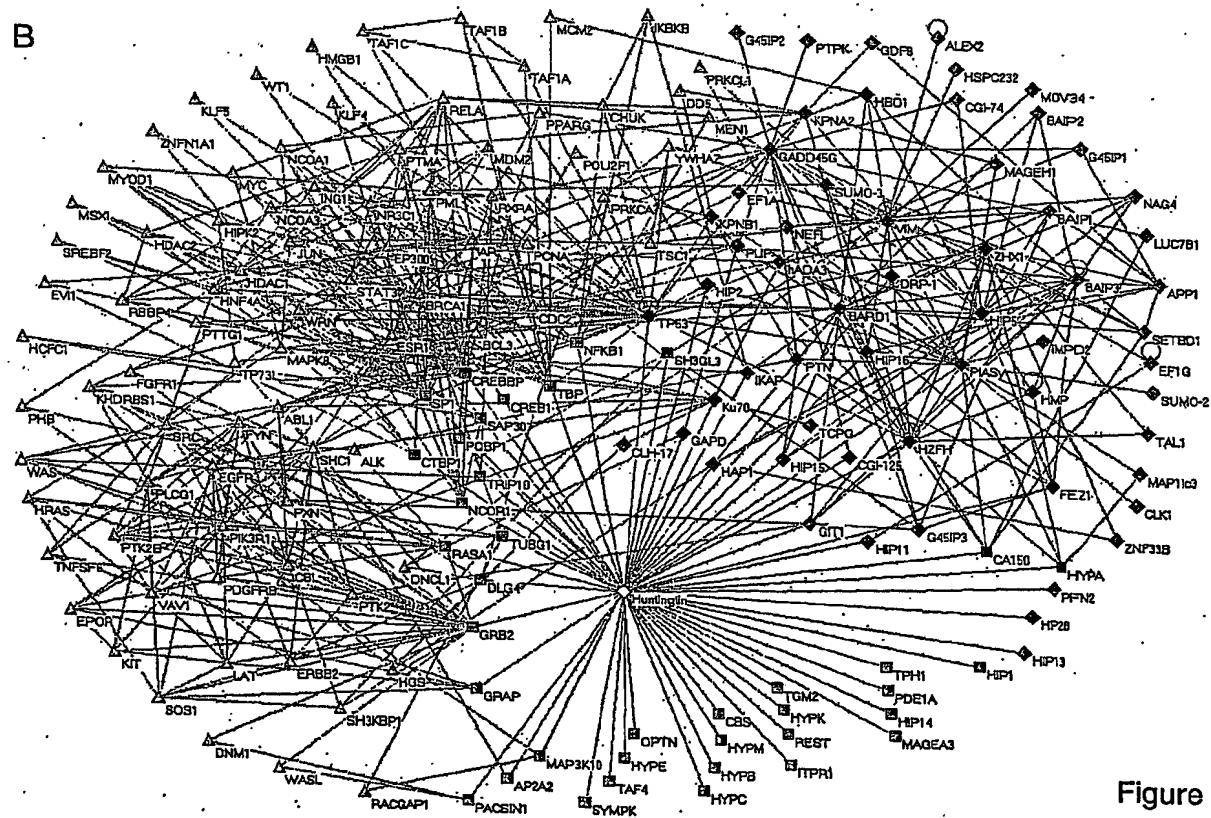


Figure 8

GST-fusion	pulled protein	beads + lysate			
		GST + lysate	GST-fusion + lysate	GST-fusion + lysate only	lysate only
CGI-125	HD510Q17	++	++	++	++
DRP-1	HD510Q17	++	++	++	++
FEZ1	HD510Q17	++	++	++	++
GIT1	HD510Q17	++	++	++	++
HZFH	HD510Q17	++	++	++	++
HIP11	HD510Q17	++	++	++	++
HIP1	HD510Q17	++	++	++	++
IKAP	HD510Q17	++	++	++	++
Ku70	HD510Q17	++	++	++	++
PFN2	HD510Q17	++	++	++	++
PIASy	HD510Q17	++	++	++	++
HIP5	HD510Q68	++	++	++	++
BARD1	GIT1	++	++	++	++
HIP5	GIT1	++	++	++	++
HZFH	GIT1	++	++	++	++
HIP15	BAIP3	++	++	++	++
GIT1	BAIP3	++	++	++	++
HIP5	HBO1	++	++	++	++
BARD1	HBO1	++	++	++	++
BARD1	HIP5	++	++	++	++
GADD45G	HIP5	++	++	++	++
SUMO-3	PIASy	++	++	++	++
hADA3	PIASy	++	++	++	++
HIP5	PLIP	++	++	++	++
GADD45G	PLIP	++	++	++	++
BARD1	CA150	++	++	++	++
BARD1	HZFH	++	++	++	++
GADD45G	HIP16	++	++	++	++
HZFH	HYPA	++	++	++	++
HIP5	FEZ1	++	++	++	++
CGI-125	GADD45G	++	++	++	++
DRP-1	VIM	++	++	++	++

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Figure 9

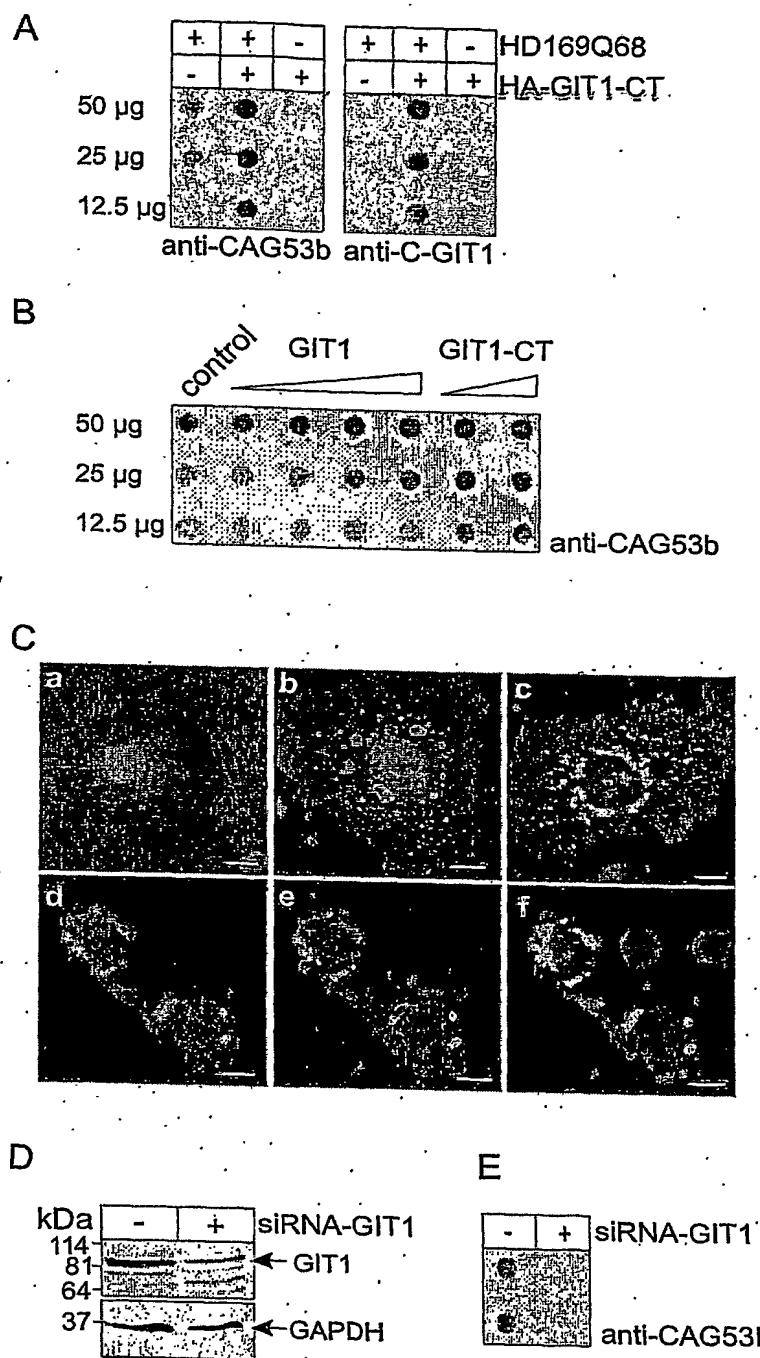


Figure 10

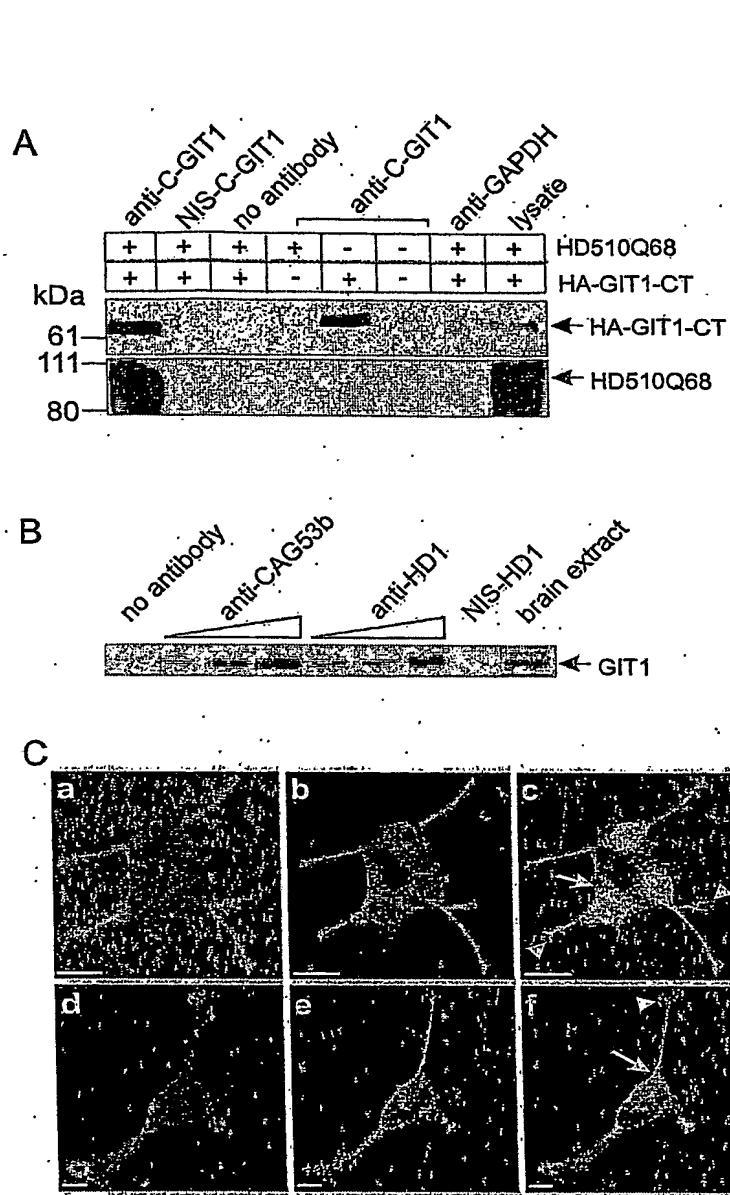


Figure 11

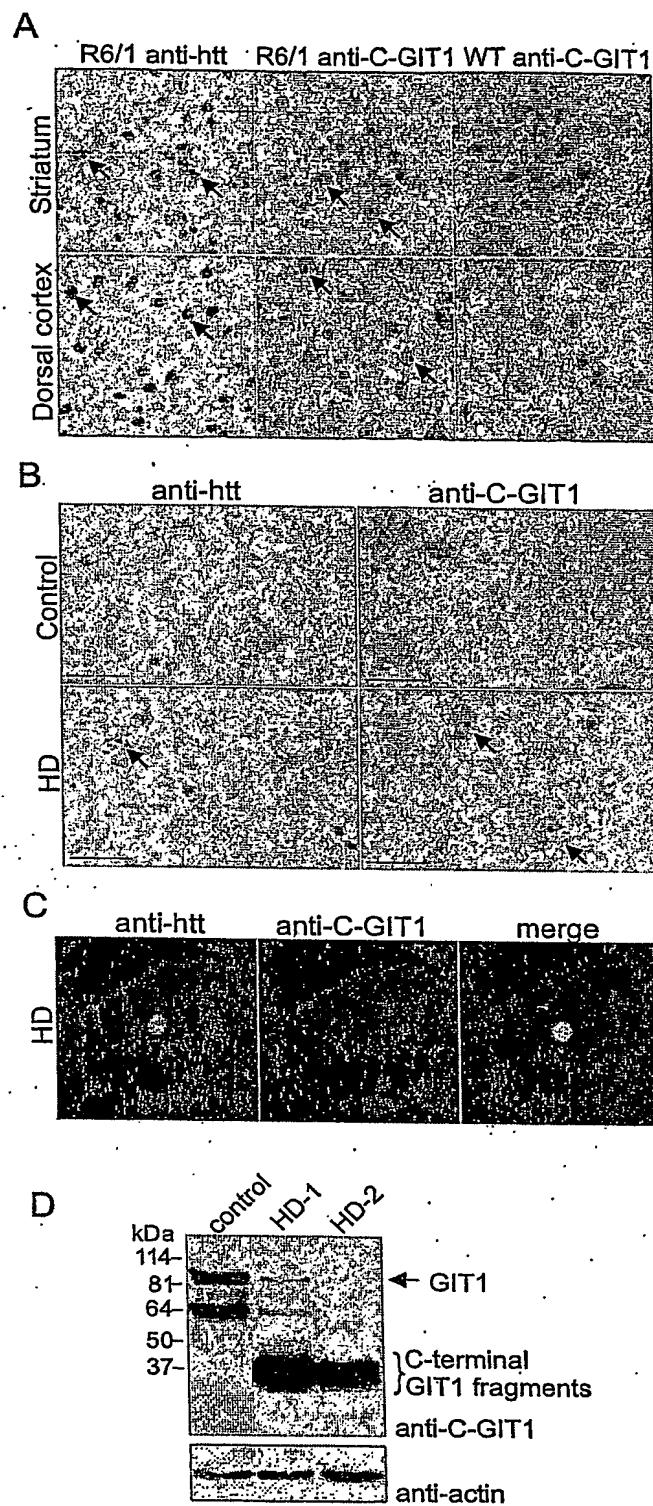


Figure 12

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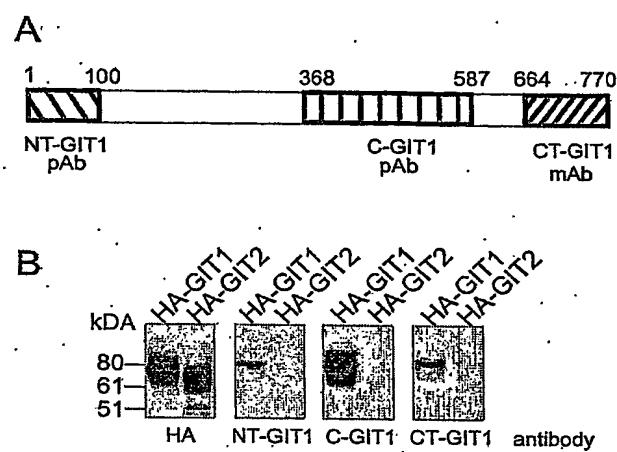


Figure 13